FIG. 1

```
GAATTCGCAG GAATTATTCA AAACATAAAC ACAATAAACA ATTTCACTAC TTCCCCCACA      60

CACACACACA CACAGCCCGT GCATTATTAC ACTAAAAGCG ACACTCAATC CAAAAAATCA     120

GCAACAAAAA CATCAATAAA C ATG CAT TGG ATT AAA TGT TTA TTA ACA GCA        171
                        Met His Trp Ile Lys Cys Leu Leu Thr Ala
                          1               5                  10

TTC ATT TGC TTC ACA GTC ATC GTC CAG GTT CAC AGT TCC GGC AGC TTT        219
Phe Ile Cys Phe Thr Val Ile Val Gln Val His Ser Ser Gly Ser Phe
                    15                  20                  25

GAG TTG CGC CTG AAG TAC TTC AGC AAC GAT CAC GGC CGG GAC AAC GAG        267
Glu Leu Arg Leu Lys Tyr Phe Ser Asn Asp His Gly Arg Asp Asn Glu
                30                  35                  40

GGT CGC TGC TGC AGC GGC GAG TCG GAC GGA GCC ACG GGC AAG TGC CTG        315
Gly Arg Cys Cys Ser Gly Glu Ser Asp Gly Ala Thr Gly Lys Cys Leu
            45                  50                  55

GGC AGC TGC AAG ACG CGG TTT CGC GTC TGC CTA AAG CAC TAC CAG GCC        363
Gly Ser Cys Lys Thr Arg Phe Arg Val Cys Leu Lys His Tyr Gln Ala
        60                  65                  70

ACC ATC GAC ACC ACC TCC CAG TGC ACC TAC GGG GAC GTG ATC ACG CCC        411
Thr Ile Asp Thr Thr Ser Gln Cys Thr Tyr Gly Asp Val Ile Thr Pro
    75                  80                  85                  90

ATT CTC GGC GAG AAC TCG GTC AAT CTG ACC GAC GCC CAG CGC TTC CAG        459
Ile Leu Gly Glu Asn Ser Val Asn Leu Thr Asp Ala Glu Arg Phe Gln
                95                  100                 105

AAC AAG GGC TTC ACG AAT CCC ATC CAG TTC CCC TTC TCG TTC TCA TGG        507
Asn Lys Gly Phe Thr Asn Pro Ile Gln Phe Pro Phe Ser Phe Ser Trp
            110                 115                 120

CCG GGT ACC TTC TCG CTG ATC GTC GAG GCC TGG CAT GAT ACG AAC AAT        555
Pro Gly Thr Phe Ser Leu Ile Val Glu Ala Trp His Asp Thr Asn Asn
        125                 130                 135

AGC GGC AAT GCG CGA ACC AAC AAG CTC CTC ATC CAG CGA CTC TTG GTG        603
Ser Gly Asn Ala Arg Thr Asn Lys Leu Leu Ile Gln Arg Leu Leu Val
    140                 145                 150

CAG CAG GTA CTG GAG GTG TCC TCC GAA TGG AAG ACG AAC AAG TCG GAA        651
Gln Gln Val Leu Glu Val Ser Ser Glu Trp Lys Thr Asn Lys Ser Glu
155                 160                 165                 170

TCG CAG TAC ACG TCG CTG GAG TAC GAT TTC CGT GTC ACC TGC GAT CTC        699
Ser Gln Tyr Thr Ser Leu Glu Tyr Asp Phe Arg Val Thr Cys Asp Leu
                175                 180                 185

AAC TAC TAC GGA TCC GGC TGT GCC AAG TTC TGC CGG CCC CGC GAC GAT        747
Asn Tyr Tyr Gly Ser Gly Cys Ala Lys Phe Cys Arg Pro Arg Asp Asp
            190                 195                 200

TCA TTT GGA CAC TCG ACT TGC TCG GAG ACG GGC GAA ATT ATC TGT TTG        795
Ser Phe Gly His Ser Thr Cys Ser Glu Thr Gly Glu Ile Ile Cys Leu
        205                 210                 215

ACC GGA TGG CAG GGC GAT TAC TGT GAC ATA CCC AAA TGC GCC AAA GGC        843
Thr Gly Trp Gln Gly Asp Tyr Cys His Ile Pro Lys Cys Ala Lys Gly
    220                 225                 230

TGT GAA CAT GGA CAT TGC GAC AAA CCC AAT CAA TGC GTT TGC CAA CTG        891
Cys Glu His Gly His Cys Asp Lys Pro Asn Gln Cys Val Cys Gln Leu
235                 240                 245                 250
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FIG. 1 CONT'D

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GGC TGC AAG GGA GCC TTG TGC AAC GAG TGC GTT CTG GAA CCG AAC TGC                939
Gly Trp Lys Gly Ala Leu Cys Asn Glu Cys Val Leu Glu Pro Asn Cys
                255                 260                 265

ATC CAT GGC ACC TGC AAC AAA CCC TGG ACT TGC ATC TGC AAC GAG GGT               987
Ile His Gly Thr Cys Asn Lys Pro Trp Thr Cys Ile Cys Asn Glu Gly
            270                 275                 280

TGG GGA GGC TTG TAC TGC AAC CAG GAT CTG AAC TAC TGC ACC AAC CAC              1035
Trp Gly Gly Leu Tyr Cys Asn Gln Asp Leu Asn Tyr Cys Thr Asn His
        285                 290                 295

AGA CCC TGC AAG AAT GGC GGA ACC TGC TTC AAC ACC GGC GAG GGA TTC              1083
Arg Pro Cys Lys Asn Gly Gly Thr Cys Phe Asn Thr Gly Glu Gly Leu
    300                 305                 310

TAC ACA TGC AAA TGC GCT CCA GGA TAC AGT GGT GAT GAT TGC GAA AAT              1131
Tyr Thr Cys Lys Cys Ala Pro Gly Tyr Ser Gly Asp Asp Cys Glu Asn
315                 320                 325                 330

GAG ATC TAC TCC TGC GAT GCC GAT GTC AAT CCC TGC CAG AAT GGT GGT              1179
Glu Ile Tyr Ser Cys Asp Ala Asp Val Asn Pro Cys Gln Asn Gly Gly
                335                 340                 345

ACC TGC ATC GAT GAG CCG CAC ACA AAA ACC GGC TAC AAG TGT CAT TGC              1227
Thr Cys Ile Asp Glu Pro His Thr Lys Thr Gly Tyr Lys Cys His Cys
            350                 355                 360

GCC AAC GGC TGG AGC GGA AAG ATG TGC GAG GAG AAA GTG CTC ACG TGT              1275
Ala Asn Gly Trp Ser Gly Lys Met Cys Glu Glu Lys Val Leu Thr Cys
        365                 370                 375

TCG GAC AAA CCC TGT CAT CAG GGA ATC TGC CGC AAC GTT CGT CCT GGC              1323
Ser Asp Lys Pro Cys His Gln Gly Ile Cys Arg Asn Val Arg Pro Gly
    380                 385                 390

TTG GGA AGC AAG GGT CAG GGC TAC CAG TGC GAA TGT CCC ATT GGC TAC              1371
Leu Gly Ser Lys Gly Gln Gly Tyr Gln Cys Glu Cys Pro Ile Gly Tyr
395                 400                 405                 410

AGC GGA CCC AAC TGC GAT CTC CAG CTG GAC AAC TGC AGT CCG AAT CCA              1419
Ser Gly Pro Asn Cys Asp Leu Gln Leu Asp Asn Cys Ser Pro Asn Pro
                415                 420                 425

TGC ATA AAC GGT GGA AGC TGT CAG CCG AGC GGA AAG TGT ATT TGC CCA              1467
Cys Ile Asn Gly Gly Ser Cys Gln Pro Ser Gly Lys Cys Ile Cys Pro
            430                 435                 440

GCC GGA TTT TCG GGA ACG AGA TGC GAG ACC AAC ATT GAC GAT TGT CTT              1515
Ala Gly Phe Ser Gly Thr Arg Cys Glu Thr Asn Ile Asp Asp Cys Leu
        445                 450                 455

GGC CAC CAG TGC GAG AAC GGA GGC ACC TGC ATA GAT ATG GTC AAC CAA              1563
Gly His Gln Cys Glu Asn Gly Gly Thr Cys Ile Asp Met Val Asn Gln
    460                 465                 470

TAT CGC TGC CAA TGC GTT CCC GGT TTC CAT GGC ACC CAC TGT AGT AGC              1611
Tyr Arg Cys Gln Cys Val Pro Gly Phe His Gly Thr His Cys Ser Ser
475                 480                 485                 490

AAA GTT GAC TTG TGC CTC ATC AGA CCC TGT GCC AAT GGA GGA ACC TGC              1659
Lys Val Asp Leu Cys Leu Ile Arg Pro Cys Ala Asn Gly Gly Thr Cys
                495                 500                 505

TTG AAT CTC AAC AAC GAT TAC CAG TGC ACC TGT CGT GCG GGA TTT ACT              1707
Leu Asn Leu Asn Asn Asp Tyr Gln Cys Thr Cys Arg Ala Gly Phe Thr
            510                 515                 520
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FIG. 1 CONT'D.

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GGC AAG GAT TGC TCT GTG GAC ATC GAT GAG TGC AGC AGT GGA CCC TGT      1755
Gly Lys Asp Cys Ser Val Asp Ile Asp Glu Cys Ser Ser Gly Pro Cys
        525                 530                 535

CAT AAC GGC GGC ACT TGC ATG AAC CGC GTC AAT TCG TTC GAA TGC GTG      1803
His Asn Gly Gly Thr Cys Met Asn Arg Val Asn Ser Phe Glu Cys Val
    540                 545                 550

TGT GCC AAT GGT TTC AGG GGC AAG CAG TGC GAT GAG GAG TCC TAC GAT      1851
Cys Ala Asn Gly Phe Arg Gly Lys Gln Cys Asp Glu Glu Ser Tyr Asp
555                 560                 565                 570

TCG GTG ACC TTC GAT GCC CAC CAA TAT GGA GCG ACC ACA CAA GCG AGA      1899
Ser Val Thr Phe Asp Ala His Gln Tyr Gly Ala Thr Thr Gln Ala Arg
                575                 580                 585

GCC GAT GGT TTG ACC AAT GCC CAG GTA GTC CTA ATT GCT GTT TTC TCC      1947
Ala Asp Gly Leu Thr Asn Ala Gln Val Val Leu Ile Ala Val Phe Ser
            590                 595                 600

GTT GCG ATG CCT TTG GTG GCG GTT ATT GCG GCG TGC GTG GTC TTC TGC      1995
Val Ala Met Pro Leu Val Ala Val Ile Ala Ala Cys Val Val Phe Cys
        605                 610                 615

ATG AAG CGC AAG CGT AAG CGT GCT CAG GAA AAG GAC GAC GCG GAG GCC      2043
Met Lys Arg Lys Arg Lys Arg Ala Gln Glu Lys Asp Asp Ala Glu Ala
    620                 625                 630

AGG AAG CAG AAC GAA CAG AAT GCG GTG GCC ACA ATG CAT CAC AAT GGC      2091
Arg Lys Gln Asn Glu Gln Asn Ala Val Ala Thr Met His His Asn Gly
635                 640                 645                 650

AGT GGG GTG GGT GTA GCT TTG GCT TCA GCC TCT CTG GGC GGC AAA ACT      2139
Ser Gly Val Gly Val Ala Leu Ala Ser Ala Ser Leu Gly Gly Lys Thr
                655                 660                 665

GGC AGC AAC AGC GGT CTC ACC TTC GAT GGC GGC AAC CCG AAT ATC ATC      2187
Gly Ser Asn Ser Gly Leu Thr Phe Asp Gly Gly Asn Pro Asn Ile Ile
            670                 675                 680

AAA AAC ACC TGG GAC AAG TCG GTC AAC AAC ATT TGT GCC TCA GCA GCA      2235
Lys Asn Thr Trp Asp Lys Ser Val Asn Asn Ile Cys Ala Ser Ala Ala
        685                 690                 695

GCA GCG GCG GCG GCG GCA GCA GCG GCG GAC GAG TGT CTC ATG TAC GGC      2283
Ala Ala Ala Ala Ala Ala Ala Ala Ala Asp Glu Cys Leu Met Tyr Gly
    700                 705                 710

GGA TAT GTG GCC TCG GTG GCG GAT AAC AAC AAT GCC AAC TCA GAC TTT      2331
Gly Tyr Val Ala Ser Val Ala Asp Asn Asn Asn Ala Asn Ser Asp Phe
715                 720                 725                 730

TGT GTG GCT CCG CTA CAA AGA GCC AAG TCG CAA AAG CAA CTC AAC ACC      2379
Cys Val Ala Pro Leu Gln Arg Ala Lys Ser Gln Lys Gln Leu Asn Thr
                735                 740                 745

GAT CCC ACG CTC ATG CAC CGC GGT TCG CCG GCA GGC AGC TCA GCC AAG      2427
Asp Pro Thr Leu Met His Arg Gly Ser Pro Ala Gly Ser Ser Ala Lys
            750                 755                 760

GGA GCG TCT GGC GGA GGA CCG GGA GCC GCG GAG GGC AAG AGG ATC TCT      2475
Gly Ala Ser Gly Gly Gly Pro Gly Ala Ala Glu Gly Lys Arg Ile Ser
        765                 770                 775

GTT TTA GGC GAG GGT TCC TAC TGT AGC CAG CGT TGG CCC TCG TTG GCG      2523
Val Leu Gly Glu Gly Ser Tyr Cys Ser Gln Arg Trp Pro Ser Leu Ala
    780                 785                 790
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FIG. 1 CONT'D.

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GCC GCC GGA GTC GCC GGA GCC TGT TCA TCC GAG CTA ATG GCT GCA GCT      2571
Ala Ala Gly Val Ala Gly Ala Cys Ser Ser Glu Leu Met Ala Ala Ala
795                 800                 805                 810

TCC GCA GCC GGC AGC GGA GCC GGG ACG GCC GAA GAG GAG AGA TCC GTC      2619
Ser Ala Ala Gly Ser Gly Ala Gly Thr Ala Glu Glu Glu Arg Ser Val
                815                 820                 825

GTC TGC GGC ACT CCG CAT ATG TAACTCCAAA AATCCCGAAC GGCTCCTCGT         2670
Val Cys Gly Thr Pro His Met
            830

AAATCCGGAC AAATCCGCAT GCAGGAGCTG ACAGCAGATA CACAAAGAAA AGACTCGGTT    2730

GGGTTCAAAA TGTGAGAGAG ACGCCAAAAT GTTGTTGTTC ATTGAAGCAC TTTAGTCGTC    2790

ACGAAAAATG AAAAATCTGT AACAGGCATA ACTCGTAAAC TCCCTAAAAA ATTTGTATAG    2850

TAATTAGCAA AGCTGTGACC CAGCCGTTTC GATCCCGAAT TC                       2892
```

FIG. 2

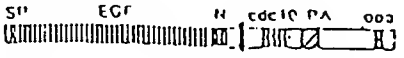
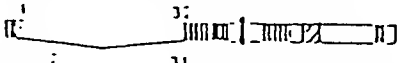
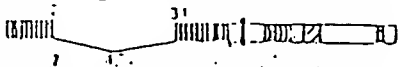
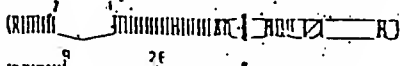
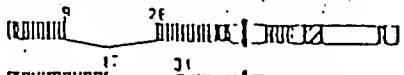
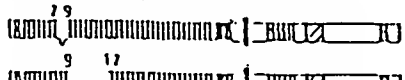
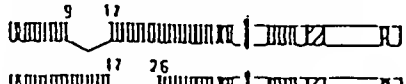
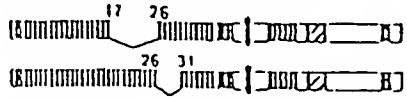
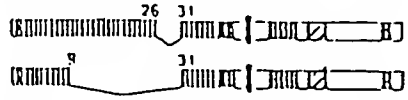
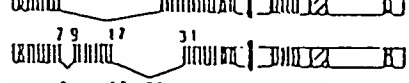
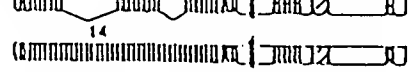
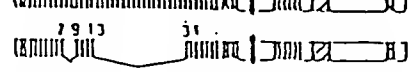
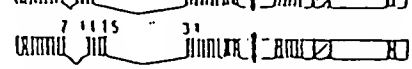
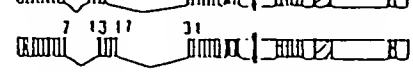
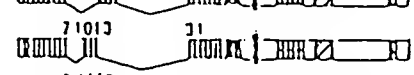
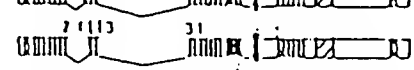
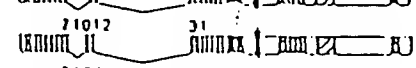
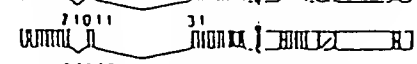
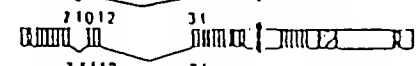
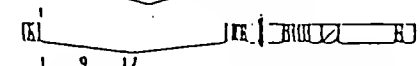
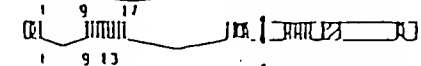
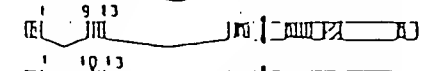
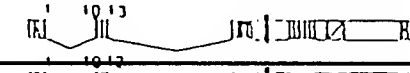
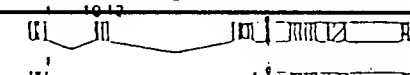
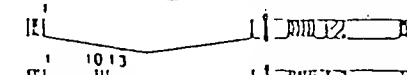
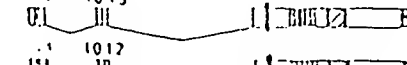
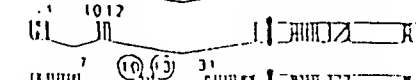
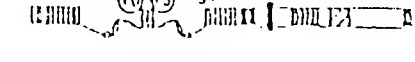
		% Aggregation with DI	% Aggregation with Ser
1. pMINMg		40	21
2. ΔSph		0	nt
3. ΔCla		0	nt
4. ΔEGF(7-17)		0	nt
5. ΔEGF(9-26)		0	nt
6. ΔEGF(17-30)		22	nt
7. ΔEGF(7-9)		20	14
8. ΔEGF(9-17)		0	0
9. ΔEGF(17-26)		10	8
10. ΔEGF(26-30)		5	7
11. ΔEGF(9-30)		0	nt
12. ΔEGF(7-26)		0	nt
13. ΔCla•EGF(9-17)		35	20
14. ΔCla•EGF(17-26)		0	nt
15. split		42	nt
16. ΔCla•EGF(9-13)		47	25
17. ΔCla•EGF(11-15)		0	0
18. ΔCla•EGF(13-17)		0	nt
19. ΔCla•EGF(10-13)		56	23
20. ΔCla•EGF(11-13)		0	nt
21. ΔCla•EGF(10-12)		0	nt
22. ΔCla•EGF(10-11)		0	nt
23. ΔCla•EGF(10-12)		45	nt
24. ΔCla•EGF(11-12)		11	nt
25. ΔEGF		0	nt
26. ΔEGF•EGF(9-17)		24	nt
27. ΔEGF•EGF(9-13)		40	nt
28. ΔEGF•EGF(10-13)		45	23
29. ΔEGF•EGF(10-12)		48	nt
30. ΔECN		0	nt
31. ΔECN•EGF(10-13)		26	nt
32. ΔECN•EGF(10-12)		47	22
33. ΔCla•XEGF(10-13)		42	20

FIG. 3

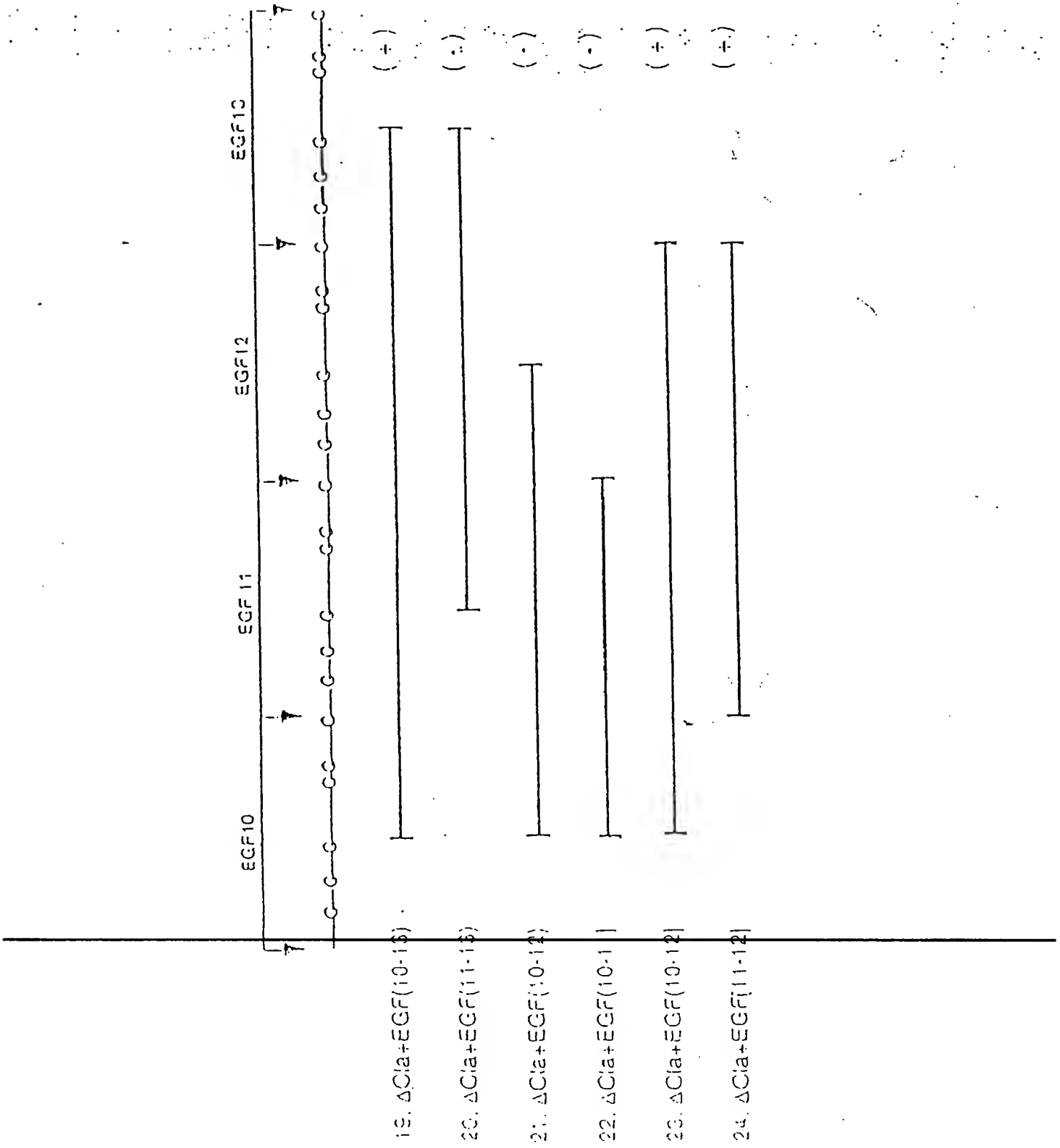


FIG. 4

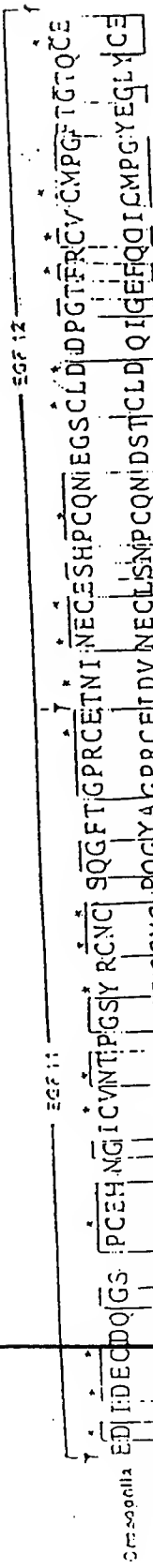


FIG. 5

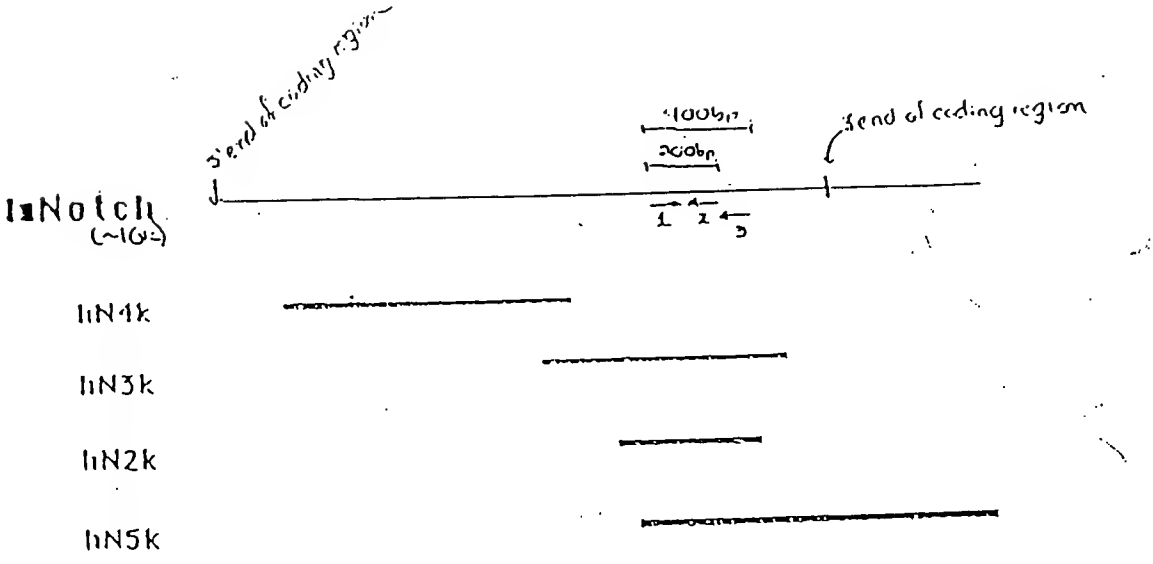
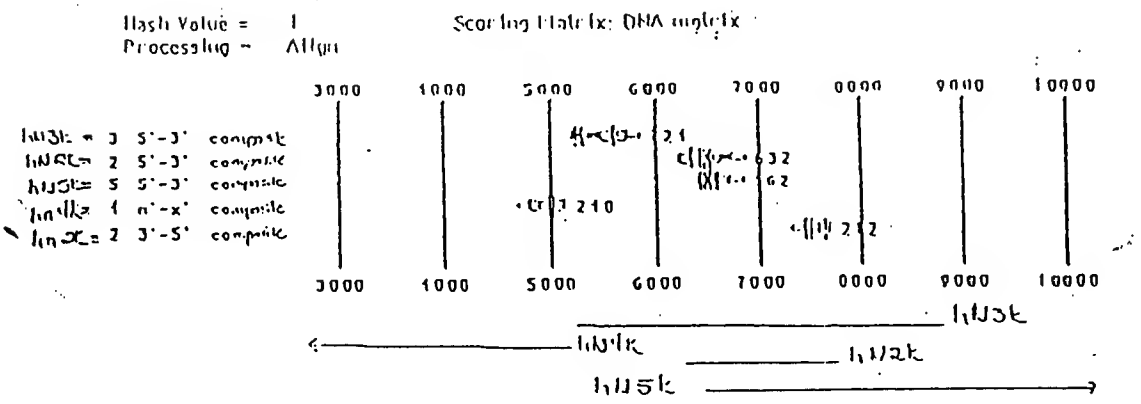

5' end of coding region
~100bp
~200bp
3' end of coding region
hNotch
(~10kb)
1
2
3
hN1k
hN3k
hN2k
hN5k

FIG. 6

FIG. 7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Processing = Align
Scoring Matrix: DNA matrix
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5000
6000
7000
8000
9000
10000
hW3k
hW1k
hW2k
hW5k

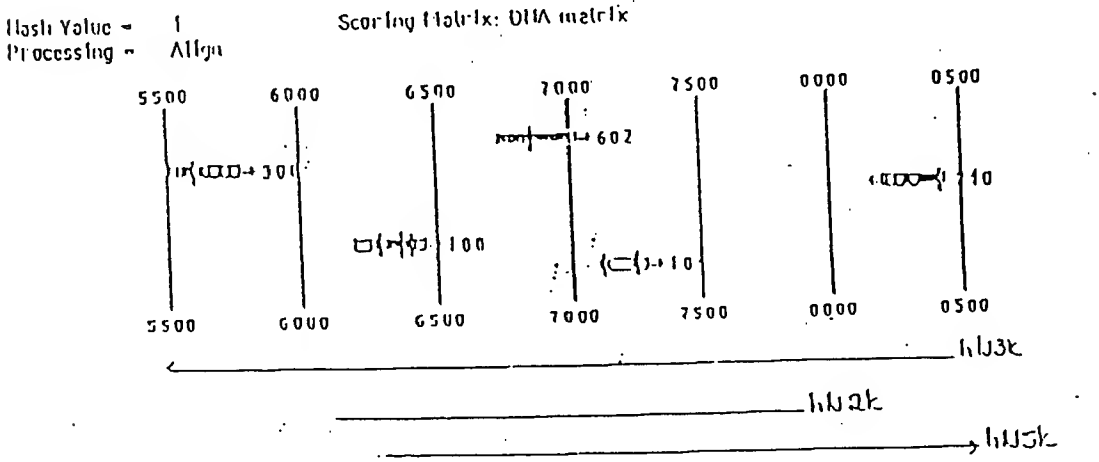
Hash Value = 1
Processing = Align
Scoring Matrix: DNA matrix
5500
6000
6500
7000
7500
8000
8500
hW3k
hW2k
hW5k

FIG. 8 A-C

A.

```
   1  GAATTCCGCT  GGGAGAATGG  TCTGAGCTAC  CTGCCCGTCC  TGCTGGGGCA  TCAATGGCAA
  61  GTGGGGAAAG  CCACACTGGG  CAAACGGGCC  AGGCCATTTC  TGGAATGTGG  TACATGGTGG
 121  GCAGGGGGCC  CGCAACAGCT  GGAGGGCAGG  TGGACTGAGG  CTGGGGATCC  CCCGCTGGTT
 181  GGGCAATACT  GCCTTTACCC  ATGAGCTGGA  AACTCACAAT  GGGGGGCAAG  GGCTCCCGAG
241  GGTGGTTATG  TGCTTCCTTC  AGGTGGC
```

B.

```
   1  GAATTCCTTC  CATTATACGT  GACTTTTCTG  AAACTGTAGC  CACCCTAGTG  TCTCTAACTC
  61  CCTCTGGAGT  TTGTCAGCTT  TGGTCTTTTC  AAAGAGCAGG  CTCTCTTCAA  GCTCCTAAAT
 121  GCGGGCATGC  TCCAGTTTGG  TCTGCGTCTC  AAGATCACCT  TTGGTAATTG  ATTCTTCTTC
 181  AACCCGGAAC  TGAAGGCTGG  CTCTCACCCT  CTAGGCAGAG  CAGGAATTCC  GAGGTGGATG
 241  TGTTAGATGT  GAATGTCCGT  GGCCCAGATG  GCTGCACCCC  ATTGATGTTG  GCTTCTCTCC
 301  GAGGAGGCAG  CTCAGATTTG  AGTGATGAAG  ATGAAGATGC  AGAGGACTGT  TCTGCTAACA
 361  TCATCACAGA  CTTGGTCTAC  CAGGGTGCCA  GCCTCCAGAC  CAGACAGACC  GGACTGGTGA
 421  GATGGCCCTG  CACCTTGCAG  CCCGCTACTC  ACGGGCTGAT  GCTGCCAAGC  GTCTCCTGGA
 481  TGCAGGTGCA  GATGCCAATG  CCCAGGACAA  CATGGGCCGC  TGTCCACTCC  ATGCTGCAGT
541  GGCACGTGAT  GCCAAGGTGT  ATTCAGATCT  GTTA
```

C.

```
   1  TCCAGATTCT  GATTCGCAAC  CGAGTAACTG  ATCTAGATGC  CAGGATGAAT  GATGGTACTA
  61  CACCCCTGAT  CCTGGCTGCC  CGCCTGGCTG  TGGAGGGAAT  GGTGGCAGAA  CTGATCAACT
 121  GCCAAGCGGA  TGTGAATGCA  GTGGATGACC  ATGGAAAATC  TGCTCTTCAC  TGGGCAGCTG
 181  CTGTCAATAA  TGTGGAGGCA  ACTCTTTTGT  TGTTCAAAAA  TGGGGCCAAC  CGAGACATGC
241  AGGACAACAA  GGAAGAGACA  CCTCTGTTTC  TTGCTGCCCG  GGAGGAGCTA  TAAGC
```

FIG. 9 A-B

A.

```
   1 GNATTCCNTT CAGGAGGNNN GGGTGGGGNG NGNNGCAGGC NCCCACTTTC CCGTGGCTGG
  61 NCTCGTTCCC NGGTGGCTCC NCCGGCNGCT GTGNCCGCCG CNGGTGGGGG CGGNGTGCCN
 121 TTCNGNNNNT TCCNGNNNNG CCCTNCCCCN NCTCGGNCGG CNNCGTCNCN CCCCTGGGTN
 181 GCNNCTGGCN CNCNNNCNGC CNGCGTGTCT GGGGCNCGGG GGGNTGGCNC CCCCTGCNGG
211 CNGNGCTG
```

B.

```
   1 CTNNNGGGNN CNNNNGCNGG NGCTCCNCCG CGGGCGGCNC NGCTCTNGNN CTNGTGGNHN
  61 NCCCGGGCTG CNGGNTTCC GGCGGNCTGG GCTCGGGCTC NGNGCGGCGC TGTGGNNGNG
 121 NTTCTNGNCC GGGNGNNCNN GCGNNTGGCT GNCNGCTGGC CTCCNNNGTC NCCNGGCTCN
 181 NNTCGCTCGC CCTGGNCNTC GNGGGNTGCN GNGGNTCNGN NCCGGTNCCT GGNTGGCNTG
 241 NCTCGGNTTT NCNNGCNTGN CCNGCCTGCT TNCNGGGNGC GTGNNNTTTT CNCNTGCNGT
301 CGNCNGNCNC GNGCTCTNTG CNT
```

FIG. 10

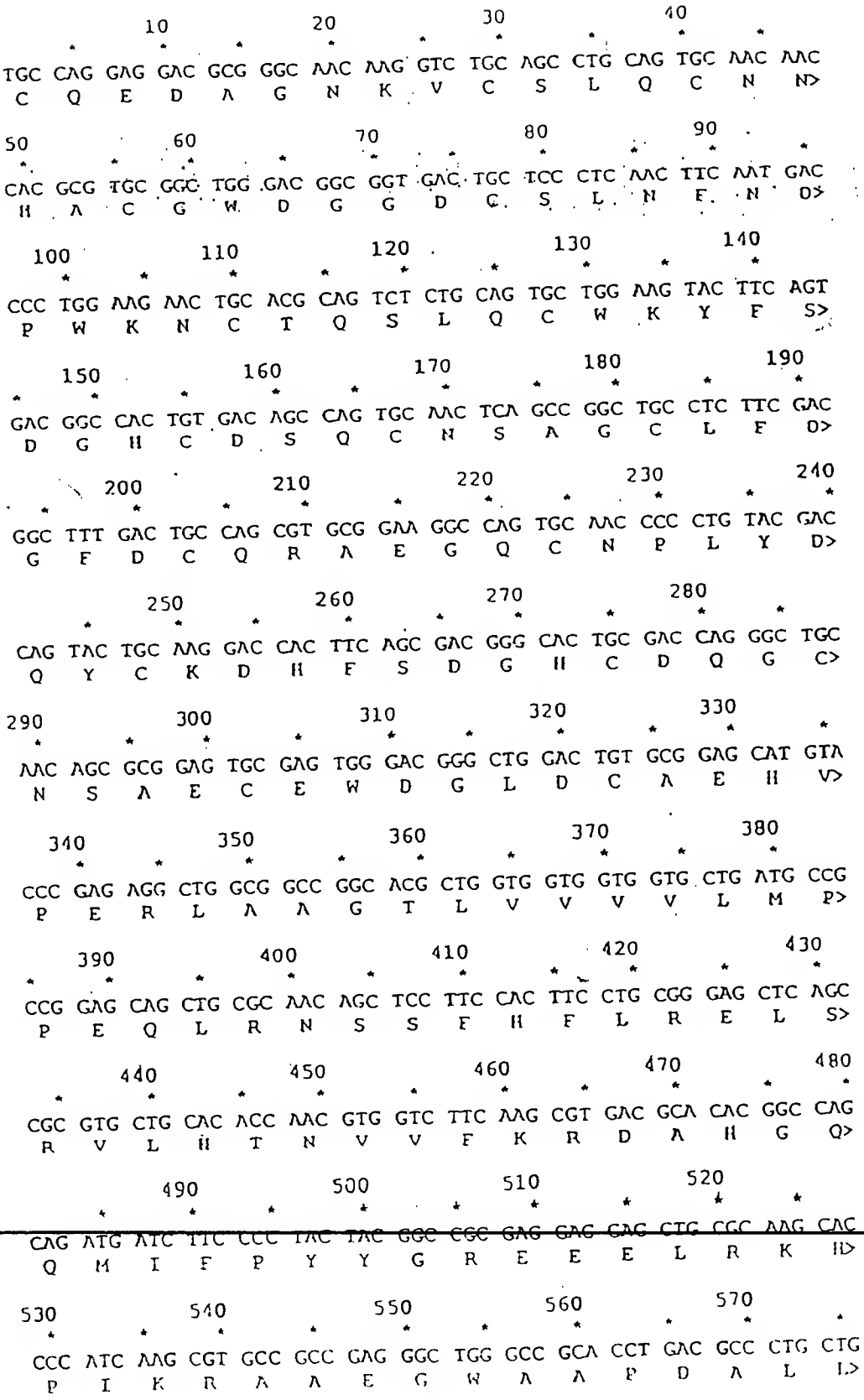

FIG. 10 CONT'D

```
580         590         600         610         620
GGC CAG GTG AAG GCC TCG CTG CTC CCT GGT GGC AGC GAG GGT GGG CGG
G   Q   V   K   A   S   L   L   P   G   G   S   E   G   G   R>

    630         640         650         660         670
CGG CGG AGG GAG CTG GAC CCC ATG GAC GTC CGC GGC TCC ATC GTC TAC
R   R   R   E   L   D   P   M   D   V   R   G   S   I   V   Y>

        680         690         700         710         720
CTG GAG ATT GAC AAC CGG CAG TGT GTG CAG GCC TCC TCG CAG TGC TTC
L   E   I   D   N   R   Q   C   V   Q   A   S   S   Q   C   F>

            730         740         750         760
CAG AGT GCC ACC GAC GTG GCC GCA TTC CTG GGA GCG CTC GCC TCG CTG
Q   S   A   T   D   V   A   A   F   L   G   A   L   A   S   L>

770         780         790         800         810
GGC AGC CTC AAC ATC CCC TAC AAG ATC GAG GCC GTG CAG AGT GAG ACC
G   S   L   N   I   P   Y   K   I   E   A   V   Q   S   E   T>

    820         830         840         850         860
GTG GAG CCG CCC CCG CCG GCG CAG CTG CAC TTC ATG TAC GTG GCG GCG
V   E   P   P   P   P   A   Q   L   H   F   M   Y   V   A   A>

        870         880         890         900         910
GCC GCC TTT GTG CTT CTG TTC TTC GTG GGC TGC GGG GTG CTG CTG TCC
A   A   F   V   L   L   F   F   V   G   C   G   V   L   L   S>

            920         930         940         950         960
CGC AAG CGC CGG CGG CAG CAT GGC CAG CTC TGG TTC CCT GAG GGC TTC
R   K   R   R   R   Q   H   G   Q   L   W   F   P   E   G   F>

        970         980         990         1000
AAA GTG TCT GAG GCC AGC AAG AAG AAG CGG CGG GAG CCC CTC GGC GAG
K   V   S   E   A   S   K   K   K   R   R   E   P   L   G   E>

1010        1020        1030        1040        1050
GAC TCC GTG GGC CTC AAG CCC CTG AAG AAC GCT TCA GAC GGT GCC CTC
D   S   V   G   L   K   P   L   K   N   A   S   D   G   A   L>

    1060        1070        1080        1090        1100
ATG GAC GAC AAC CAG AAT GAG TGG GGG GAC GAG GAC CTG GAG ACC AAG
M   D   D   N   Q   N   E   W   G   D   E   D   L   E   T   K>

    1110        1120        1130        1140        1150
AAG TTC CGG TTC GAG GAG CCC GTG GTT CTG CCT GAC CTG GAC GAC CAG
K   F   R   F   E   E   P   V   V   L   P   D   L   D   D   Q>

        1160        1170        1180        1190        1200
```

FIG. 10 CONT'D

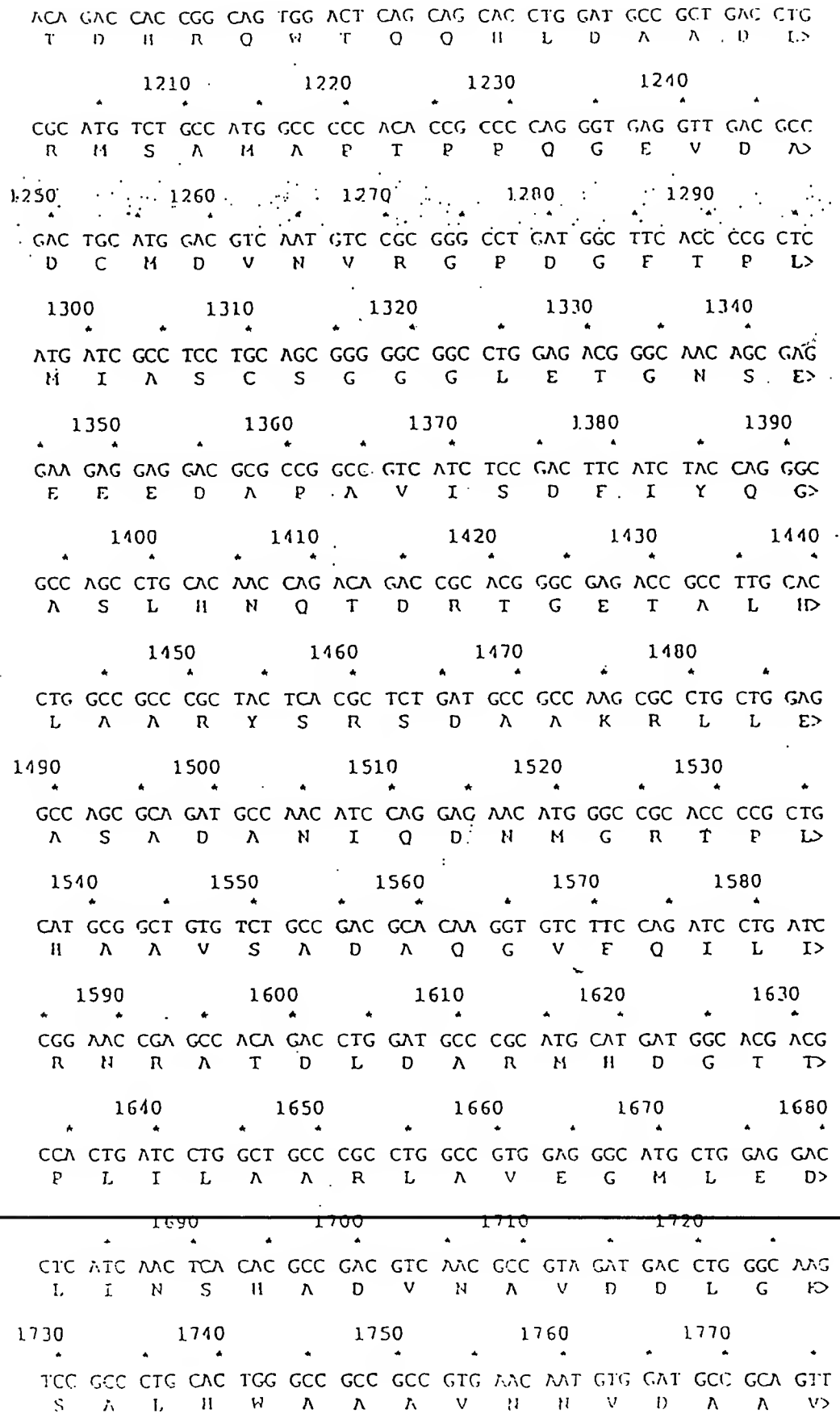

FIG. 10 CONT'D

```
1780        1790        1800        1810        1820
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GTG CTC CTG AAG AAC GGG GCT AAC AAA GAT ATG CAG AAC AAC AGG GAG
 V   L   L   K   N   G   A   N   K   D   M   Q   N   N   R   E>

1830        1840        1850        1860        1870
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GAG ACA CCC CTG TTT CTG GCC GCC CGG GAG GGC AGC TAC GAG ACC GCC
 E   T   P   L   F   L   A   A   R   E   G   S   Y   E   T   A>

1880        1890        1900        1910        1920
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
AAG GTG CTG CTG GAC CAC TTT GCC AAC CGG GAC ATC ACG GAT CAT ATG
 K   V   L   L   D   H   F   A   N   R   D   I   T   D   H   M>

1930        1940        1950        1960
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GAC CGC CTG CCG CGC GAC ATC GCA CAG GAG CGC ATG CAT CAC GAC ATC
 D   R   L   P   R   D   I   A   Q   E   R   M   H   H   D   I>

1970        1980        1990        2000        2010
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GTG AGG CTG CTG GAC GAG TAC AAC CTG GTG CGC AGC CCG CAG CTG CAC
 V   R   L   L   D   E   Y   N   L   V   R   S   P   Q   L   H>

2020        2030        2040        2050        2060
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GGA GCC CCG CTG GGG GGC ACG CCC ACC CTG TCG CCC CCG CTC TGC TCG
 G   A   P   L   G   G   T   P   T   L   S   P   P   L   C   S>

2070        2080        2090        2100        2110
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CCC AAC GGC TAC CTG GGC AGC CTC AAG CCC GGC GTG CAG GGC AAG AAG
 P   N   G   Y   L   G   S   L   K   P   G   V   Q   G   K   K>

2120        2130        2140        2150        2160
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GTC CGC AAG CCC AGC AGC AAA GGC CTG GCC TGT GGA AGC AAG GAG GCC
 V   R   K   P   S   S   K   G   L   A   C   G   S   K   E   A>

2170        2180        2190        2200
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
AAG GAC CTC AAG GCA CGG AGG AAG AAG TCC CAG GAT GGC AAG GGC TGC
 K   D   L   K   A   R   R   K   K   S   Q   D   G   K   G   C>

2210        2220        2230        2240        2250
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CTG CTG GAC AGC TCC GGC ATG CTC TCG CCC GTG GAC TCC CTG GAG TCA
 L   L   D   S   S   G   M   L   S   P   V   D   S   L   E   S>

2260        2270        2280        2290        2300
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CCC CAT GGC TAC CTG TCA GAC GTG GCC TCG CCG CCA CTG CTG CCC TCC
 P   H   G   Y   L   S   D   V   A   S   P   P   L   L   P   S>

2310        2320        2330        2340        2350
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CCG TTC CAG CAG TCT CCG TCC GTG CCC CTC AAC CAC CTG CCT GGG ATG
 P   F   Q   Q   S   P   S   V   P   L   N   H   L   P   G   M>

2360        2370        2380        2390        2400
```

FIG. 10 CONT'D

```
                                                                    *
CCC GAC ACC CAC CTG GGC ATC GGG CAC CTG AAC GTG GCG GCC AAG CCC
 P   D   T   H   L   G   I   G   H   L   N   V   A   A   K   P>

        2410        2420        2430        2440
         *           *           *           *           *
GAG ATG GCG GCG CTG GGT GGG GGC GGC CGG GTG GCC TTT GAG ACT GGC
 E   M   A   A   L   G   G   G   G   R   L   A   F   E   T   G>

2450        2460        2470        2480        2490
 *           *           *           *           *           *
CCA CCT CGT CTC TCC CAC CTG CCT GTG GCC TCT GGC ACC AGC ACC GTC
 P   P   R   L   S   H   L   P   V   A   S   G   T   S   T   V>

  2500        2510        2520        2530        2540
   *           *           *           *           *           *
CTG GGC TCC AGC AGC GGA GGG GCC CTG AAT TTC ACT GTG GGC GGG TCC
 L   G   S   S   S   G   G   A   L   N   F   T   V   G   G   S>

    2550        2560        2570        2580        2590
     *           *           *           *           *           *
ACC AGT TTG AAT GGT CAA TGC GAG TGG CTG TCC CGG CTG CAG AGC GGC
 T   S   L   N   G   Q   C   E   W   L   S   R   L   Q   S   G>

      2600        2610        2620        2630        2640
       *           *           *           *           *           *
ATG GTG CCG AAC CAA TAC AAC CCT CTG CGG GGG AGT GTG GCA CCA GGC
 M   V   P   N   Q   Y   N   P   L   R   G   S   V   A   P   G>

        2650        2660        2670        2680
         *           *           *           *           *
CCC CTG AGC ACA CAG GCC CCC TCC CTG CAG CAT GGC ATG GTA GGC CCG
 P   L   S   T   Q   A   P   S   L   Q   H   G   M   V   G   P>

2690        2700        2710        2720        2730
 *           *           *           *           *           *
CTG CAC AGT AGC CTT GCT GCC AGC GCC CTG TCC CAG ATG ATG AGC TAC
 L   H   S   S   L   A   A   S   A   L   S   Q   M   M   S   Y>

  2740        2750        2760        2770        2780
   *           *           *           *           *           *
CAG GGC CTG CCC AGC ACC CGG CTG GCC ACC CAG CCT CAC CTG GTG CAG
 Q   G   L   P   S   T   R   L   A   T   Q   P   H   L   V   Q>

    2790        2800        2810        2820        2830
     *           *           *           *           *           *
ACC CAG CAG GTG CAG CCA CAA AAC TTA CAG ATG CAG CAG CAG AAC CTG
 T   Q   Q   V   Q   P   Q   N   L   Q   M   Q   Q   Q   N   L>

      2840        2850        2860        2870        2880
       *           *           *           *           *           *
CAG CCA GCA AAC ATC CAG CAG CAG CAA AGC CTG CAG CCG CCA CCA CCA
 Q   P   A   N   I   Q   Q   Q   Q   S   L   Q   P   P   P   P>

        2890        2900        2910        2920
         *           *           *           *           *
CCA CCA CAG CCG CAC CTT GGC GTG AGC TCA GCA GCC AGC GGC CAC CTG
 P   P   Q   P   H   L   G   V   S   S   A   A   S   G   H   L>

2930        2940        2950        2960        2970
 *           *           *           *           *           *
GGC CGG AGC TTC CTG AGT GGA GAG CCG AGC CAG GCA GAC GTG CAG CCA
```

FIG. 10 CONT'D

```
 G   R   S   F   L   S   G   E   P   S   Q   A   D   V   Q   P>

 2980        2990        3000        3010        3020
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CTG GGC CCC AGC AGC CTG GCG GTG CAC ACT ATT CTG CCC CAG GAG AGC
 L   G   P   S   S   L   A   V   H   T   I   L   P   Q   E   S>

    3030        3040        3050        3060        3070
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CCC GCC CTG CCC ACG TCG CTG CCA TCC TCG CTG GTC CCA CCC GTG ACC
 P   A   L   P   T   S   L   P   S   S   L   V   P   P   V   T>

        3080        3090        3100        3110        3120
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GCA GCC CAG TTC CTG ACG CCC CCC TCG CAG CAC AGC TAC TCC TCG CCT
 A   A   Q   F   L   T   P   P   S   Q   H   S   Y   S   S   P>

            3130        3140        3150        3160
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GTG GAC AAC ACC CCC AGC CAC CAG CTA CAG GTG CCT GTT CCT GTA ATG
 V   D   N   T   P   S   H   Q   L   Q   V   P   V   P   V   M>

3170        3180        3190        3200        3210
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GTA ATG ATC CGA TCT TCG GAT CCT TCT AAA GGC TCA TCA ATT TTG ATC
 V   M   I   R   S   S   D   P   S   K   G   S   S   I   L   I>

    3220        3230
  *   *   *   *   *
GAA GCT CCC GAC TCA TGG
 E   A   P   D   S   W>
```

FIG. 11

```
C GAG GTC GAT GTC TTA GAT GTG AAT GTC CGT GGC CCA GAT GGC TGC          46
  Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys
    1               5                  10                  15

ACC CCA TTG ATG TTG GCT TCT GTC CGA GGA GGC AGC TCA GAT TTG AGT        94
Thr Pro Leu Met Leu Ala Ser Leu Arg Gly Gly Ser Ser Asp Leu Ser
            20                  25                  30

GAT GAA GAT GAA GAT GCA GAG GAC TCT TCT GCT AAC ATC ATC ACA GAC        142
Asp Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp
        35                  40                  45

TTG GTC TAC GAG GGT GCC AGC CTG GAG GCC GAG ACA GAC CGC ACT GGT        190
Leu Val Tyr Glu Gly Ala Ser Leu Glu Ala Glu Thr Asp Arg Thr Gly
    50                  55                  60

GAG ATG GCC CTG CAC CTT GCA GCC CGC TAC TCA CGG GCT GAT GCT GCC        238
Glu Met Ala Leu His Leu Ala Ala Arg Tyr Ser Arg Ala Asp Ala Ala
65                  70                  75

AAG CGT CTG CTG GAT GCA GGT GCA GAT GCC AAT GCC CAG GAC AAC ATG        286
Lys Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Glu Asp Asn Met
80                  85                  90                  95

GGC CGC TGT CCA CTC CAT GCT GCA GTG GCA GCT GAT GCC CAA GGT GTC        334
Gly Arg Cys Pro Leu His Ala Ala Val Ala Ala Asp Ala Glu Gly Val
            100                 105                 110

TTC CAG ATT CTG ATT CGC AAC CGA GTA ACT GAT CTA GAT GCC AGG ATG        382
Phe Gln Ile Leu Ile Arg Asn Arg Val Thr Asp Leu Asp Ala Arg Met
        115                 120                 125

AAT GAT GGT ACT ACA CCC CTG ATC CTG GCT GCC CGC CTG GCT GTG GAG        430
Asn Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu
    130                 135                 140

GGA ATG GTG GCA GAA CTG ATC AAC TGC CAA GCG GAT GTG AAT GCA GTC        478
Gly Met Val Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val
145                 150                 155

GAT GAC GAT GGA AAA TCT GCT CTT CAC TGG GCA GCT GCT GTC AAT AAT        526
Asp Asp Asp Gly Lys Ser Ala Leu His Trp Ala Ala Ala Val Asn Asn
160                 165                 170                 175

GTG GAG GCA ACT CTT TTG TTG TTG AAA AAT GGG GCC AAC CGA GAC ATG        574
Val Glu Ala Thr Leu Leu Leu Leu Lys Asn Gly Ala Asn Arg Asp Met
            180                 185                 190

CAG GAC AAC AAG GAA GAG ACA CCT CTG TTT CTT GCT GCC CGG GAG GGC        622
Gln Asp Asn Lys Glu Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly
        195                 200                 205

AGC TAT GAA GCA GCC AAG ATC CTG TTA GAC CAT TTT GCC AAT CGA GAC        670
Ser Tyr Glu Ala Ala Lys Ile Leu Leu Asp His Phe Ala Asn Arg Asp
    210                 215                 220

ATC ACA GAC CAT ATG GAT CGT CTT CCC CGG GAT GTG GCT CGG GAT CGC        718
Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp Val Ala Arg Asp Arg
225                 230                 235

ATG CAC CAT CAC ATT GTG CGC CTT CTG GAT GAA TAC AAT GTG ACC CCA        766
Met His His Asp Ile Val Arg Leu Leu Asp Glu Tyr Asn Val Thr Pro
240                 245                 250                 255
```

FIG. 11 CONT'D

```
AGC CCT CCA GGC ACC GTC TTG ACT TCT GCT CTC TCA CCT GTC ATC TGT                 814
Ser Pro Pro Gly Thr Val Leu Thr Ser Ala Leu Ser Pro Val Ile Cys
                260                 265                 270

GGC CCC AAC AGA TCT TTC CTC AGC CTC AAG CAC ACC CCA ATG GGC AAG                862
Gly Pro Asn Arg Ser Phe Leu Ser Leu Lys His Thr Pro Met Gly Lys
            275                 280                 285

AAG TCT AGA CGC CCC AGT GCC AAC ACT ACC ATC GCT ACT AGC CTC CCT                910
Lys Ser Arg Arg Pro Ser Ala Lys Ser Thr Ile Ala Thr Ser Leu Pro
        290                 295                 300

AAC CTT GCC AAG GAG GCA AAG GAT GCC AAG GCT AGT AGG AGG AAG AAG                958
Asn Leu Ala Lys Glu Ala Lys Asp Ala Lys Gly Ser Arg Arg Lys Lys
    305                 310                 315

TCT CTC AGT GAG AAG GTC GAA CTG TCT GAG AGT TCA GTA ACT TTA TCC               1006
Ser Leu Ser Glu Lys Val Glu Leu Ser Glu Ser Ser Val Thr Leu Ser
320                 325                 330                 335

CCT GTT GAT TCC CTA GAA TCT CCT GAC ACC TAT GTT TCC GAC AGC AGA               1054
Pro Val Asp Ser Leu Glu Ser Pro His Thr Tyr Val Ser Asp Thr Thr
                340                 345                 350

TCC TCT CCA ATG ATT ACA TCC CCT GGG ATC TTA CAG GCC TCA CCC AAC               1102
Ser Ser Pro Met Ile Thr Ser Pro Gly Ile Leu Gln Ala Ser Pro Asn
            355                 360                 365

CCT ATG TTG GCC ACT GCC GCC CCT CCT GCC CCA GTC CAT GCC CAG CAT               1150
Pro Met Leu Ala Thr Ala Ala Pro Pro Ala Pro Val His Ala Gln His
        370                 375                 380

GCA CTA TCT TTT TCT AAC CTT CAT GAA ATG CAG CCT TTG GCA CAT GGC               1198
Ala Leu Ser Phe Ser Asn Leu His Glu Met Gln Pro Leu Ala His Gly
    385                 390                 395

GCC AGC ACT GTG CTT CCC TCA GTC AGC CAG TTG CTA TCC CAC CAC CAC               1246
Ala Ser Thr Val Leu Pro Ser Val Ser Gln Leu Leu Ser His His His
400                 405                 410                 415

ATT GTC TCT CCA GGC AGT GGC AGT GCT GGA AGC TTG AGT AGG CTC CAT               1294
Ile Val Ser Pro Gly Ser Gly Ser Ala Gly Ser Leu Ser Arg Leu His
                420                 425                 430

CCA GTC CCA GTC CCA GCA GAT TGG ATG AAC CGC ATG CAG GTC AAT GAG               1342
Pro Val Pro Val Pro Ala Asp Trp Met Asn Arg Met Gln Val Asn Glu
            435                 440                 445

ACC CAG TAC AAT GAG ATG TTT GGT ATG GTC CTC GCT CCA GCT GAG GGC               1390
Thr Gln Tyr Asn Glu Met Phe Gly Met Val Leu Ala Pro Ala Glu Gly
        450                 455                 460

ACC CAT CCT GGC ATA GCT CCC CAG AGC AGG CCA CCT CCA GAA GGC AAG CAC           1438
Thr His Pro Gly Ile Ala Pro Gln Ser Arg Pro Pro Glu Gly Lys His
    465                 470                 475

ATA ACC ACC CCT CGC GAG CCC TTG CCC CCC ATT CTC ACT TTC CAG CTC               1486
Ile Thr Thr Pro Arg Glu Pro Leu Pro Pro Ile Val Thr Phe Gln Leu
480                 485                 490                 495

ATC CCT AAA GGC AGT ATT GCC CAA CCA GCC GGC GCT CCC CAG CCT CAG               1534
Ile Pro Lys Gly Ser Ile Ala Gln Pro Ala Gly Ala Pro Gln Pro Gln
                500                 505                 510

TCC ACC TGC CCT CCA GCT GTT GCG GGC CCC CTG CCC ACC ATC TAC CAG               1582
Ser Thr Cys Pro Pro Ala Val Ala Gly Pro Leu Pro Thr Met Tyr Gln
            515                 520                 525

ATT CCA GAA ATG GCT GCT TTG CCC AGT GTC GCT TTC CCC ACT GCC ATG               1630
Ile Pro Glu Met Ala Arg Leu Pro Ser Val Ala Phe Pro Thr Ala Met
        530                 535                 540
```

FIG. 11 CONT'D

```
ATG CCC GAG CAG GAC GGG CAG GTA GCT CAG ACC ATT CTG CCA GCC TAT      1670
Met Pro Glu Glu Asp Gly Gln Val Ala Glu Thr Ile Leu Pro Ala Tyr
    545                 550                 555

CAT CCT TTC CCA GCC TCT GTG GGG AAG TAC CCC ACA CCC CCT TCA CAC      1726
His Pro Phe Pro Ala Ser Val Gly Lys Tyr Pro Thr Pro Pro Ser Glu
560                 565                 570                 575

CAC AGT TAT GCT TCC TCA AAT GCT GCT GAG CGA ACA CCC AGT CAC AGT      1774
His Ser Tyr Ala Ser Ser Asn Ala Ala Glu Arg Thr Pro Ser His Ser
                580                 585                 590

GGT CAC CTC CAG GGT GAG CAT CCC TAC CTG ACA CCA TCC CCA GAG TCT      1822
Gly His Leu Gln Gly Glu His Pro Tyr Leu Thr Pro Ser Pro Glu Ser
            595                 600                 605

CCT GAC CAG TGG TCA AGT TCA TCA CCC CAC TCT GCT TCT GAC TGG TCA      1870
Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser Ala Ser Asp Trp Ser
        610                 615                 620

GAT GTG ACC AGC AGC CCT ACC CCT GGG GCT GCT GGA GGA GGT CAG CGG      1918
Asp Val Thr Thr Ser Pro Thr Pro Gly Gly Ala Gly Gly Gly Gln Arg
    625                 630                 635

GGA CCT GGG ACA CAC ATG TCT GAG CCA CCA CAC AAC AAC ATG CAG GTT      1966
Gly Pro Gly Thr His Met Ser Glu Pro Pro His Asn Asn Met Gln Val
640                 645                 650                 655

TAT GCC TGAGAGAGTC CACCTCCAGT GTAGAGACAT AACTGACTTT TGTAAAATGCT      2022
Tyr Ala

GCTGAGGAAC AAATGAAGGT CATCCGGGAG AGAAATGAAG AAATCTCTGG AGCCAGCTTC    2082

TAGAGGTAGG AAAGAGAAGA TGTTCTTATT CAGATAATGC AAGAGAAGCA ATTCGTCAGT    2142

TTCACTGGGT ATCTGCAAGG CTTATTGATT ATTCTAATCT AATAAGACAA GTTTGTGGAA    2202

ATGCAAGATG AATACAAGCC TTGGGTCCAT GTTTACTCTC TTCTATTTGG AGAATAAGAT    2262

GGATGCTTAT TGAAGCCCAG ACATTCTTGC AGCTTGGACT GCATTTTAAG CCCTGCAGGC    2322

TTCTGCCATA TCCATGAGAA GATTCTACAG TAGCGTCCTG TTGGGAATTA TGCCCTGGAA    2382

TTCTGCCTGA ATTGACCTAC GCATCTCCTC CTCCTTGGAC ATTCTTTTGT CTTCATTTGG    2442

TGCTTTTGGT TTTGCACCTC TCCGTGATTG TAGCCCTACC AGCATGTTAT AGGGCAAGAC    2502

CTTTGTGCTT TTGATCATTC TGGCCCATGA AAGCAACTTT GGTCTCCTTT CCCCTCCTGT    2562

CTTCCCCGTA TCCCTTGGAG TCTCAGAAGG TTTACTTTGG TATGGTTCTC AGCACAAACC    2622

TTTCAAGTAT GTTGTTTCTT TGGAAAATGG AGATACTGTA TTGTGTTCTC CTGCATATAT    2682

CATTCCTGGA GAGAGAAGGG GAGAAGAATA CTTTTCTTCA ACAAATTTTG GGGGCAGGAG    2742

ATCGGTTCAA GAGGCTGCAC CTTAATTTTT CTTGTCTGTG TGCAGGTCTT CATATAAACT    2802

TTACCAGGAA GAAGGGTGTG AGTTTGTTGT TTTTCTGTGT ATGGGCCTGG TCAGTGTAAA    2862

GTTTTATCCT TGATAGTCTA GTTAGTATGA CCCTCCCCAC TTTTTTAAAA CCAGAAAAAG    2922

GTTTGGAATG TTGGAAATGAC CAAGAGAGAA GTTAACTCGT GCAAGAGCCA GTTAGCCACC    2982

CAGAGGTCCC CCTACTTCCT GCCAAGCATT CCATTGACTG CCTGTATGGA AGACATTTGT    3042

CCCAGATCTG AGCATTCTAG GCCTGTTTCA CTCACTCACC CAGCATATGA AAGTAGTCTT    3102

AAGTGTTGAG CCTTTCGTTT CATATCCAGA GAAGAGACTG TGTCAAAATGT TGTAGCCTTC    3162
```

FIG. 11 CONT'D

GCATTTAGGA CTGAACTTTC CTTAGCCCAA GGGACCCAGT GACAGTTGTC TTCCGTTTGT	3222
CAGATGATGA GTCTCTACTG ATTATGTTGC TGCTTAAAGG CCTGGTGACC AATCTTTCTT	3282
TCACACCCTG TGGTCCGTGT TACTGGTATA CGCAGTATGT TCTGACTGAA GACATGGACT	3342
TTATATGTTC AAGTGCAGGA ATTGGAAAGT TGGAGTTGTT TTCTATGATC CAAAACAGCC	3402
CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT	3462
TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG	3522
AACATTTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GAGAACTATA GACTTGCTCA	3582
TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCAGTCTCTG TATTCATGCT CTTGGCAATT	3642
TCTTTGACTT TCTTTTAAGG GCAGAAGCAT TTTAGTTAAT TGTAGATAAA GAATAGTTTT	3702
CTTGCTCTTC TGCTTGGGGC AGTTAATAAT TGGTCCATGC CTACAGTGCA ACTTCCGTCC	3762
ACTGCTGTGA TGCCCATGAC ACCTGCAAAA TAAGTTCTGC CTGGGCATTT TGTAGATATT	3822
AACAGGTGAA TTCCCGACTC TTTTGGTTTG AATGACAGTT CTCATTCCTT CTATGGCTGC	3882
AAGTATGCAT CAGTGCTTCC CACTTACCTG ATTTGTCTGT CGGTGGCCCC ATATGGAAAC	3942
CCTGCGTGTC TGTTGGCATA ATAGTTTACA AATGGTTTTT TCAGTCCTAT CCAAATTTAT	4002
TGAACCAACA AAAATAATTA CTTCTGCCCT GAGATAAGCA GATTAAGTTT GTTCATTCTC	4062
TGCTTTATTC TGTCCATGTG GCAACATTCT GTCAGCCTCT TTCATAGTGT GCAAACATTT	4122
TATCATTCTA AATGGTGACT CTCTGCCCTT GGACCCATTT ATTATTCACA GATGGGGAGA	4182
ACCTATCTGC ATGGACCCTG ACCATCCTCT GTGCAGCACA CACAGTGCAG GGAGCCAGTG	4242
GCGATGGCGA TGAGTTTCTT CCCCTG	4268

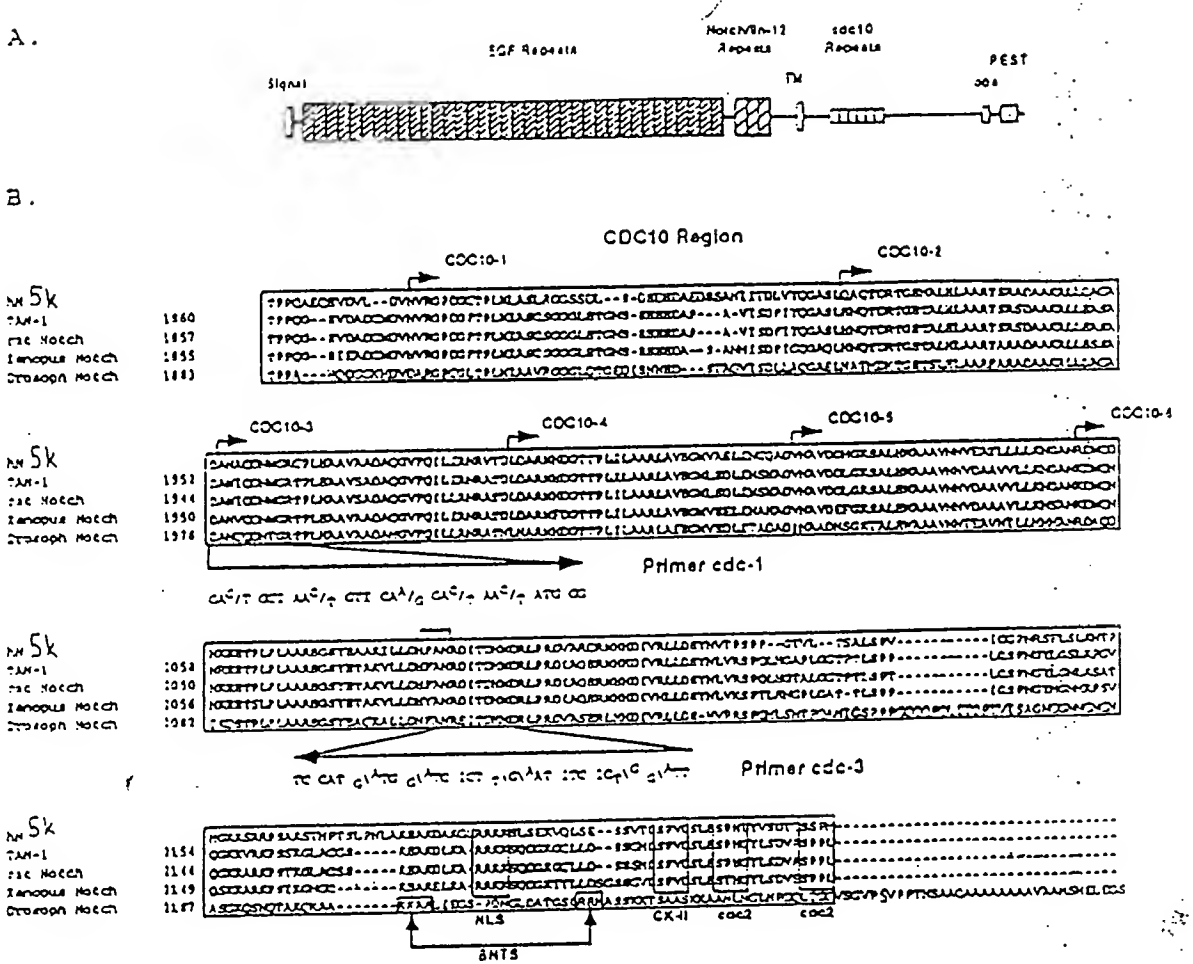
A.
EGF Repeats
Notch/Lin-12 Repeats
cdc10 Repeats
Signal
TM
PEST
B.
CDC10 Region
CDC10-1
CDC10-2
CDC10-3
CDC10-4
CDC10-5
CDC10-6
Primer cdc-1
Primer cdc-3
NLS
CK-II
cdc2
cdc2
ANTS

FIG. 12 A-B

FIG. 12B CONT'D

FIG.13

FIG. 13 CONT'D

LNR (Notch/Lin-12 Repeats)
TM
CDC-10/Ankyrin Repeats
NLS
CK II
cdc2
cdc2
BNTS

FIG. 13 CONT'D

FIG. 14

FIG. 15A

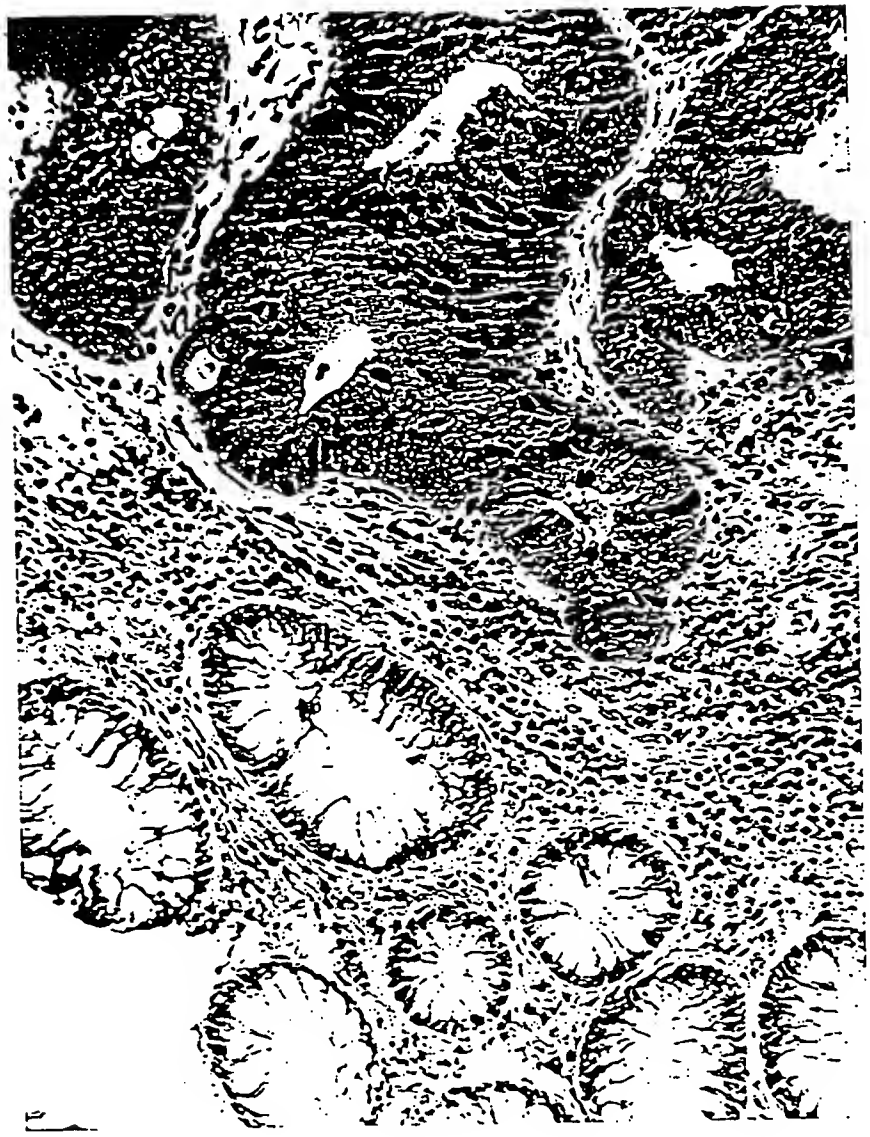

FIG. 15B

FIG. 16A

FIG. 16B

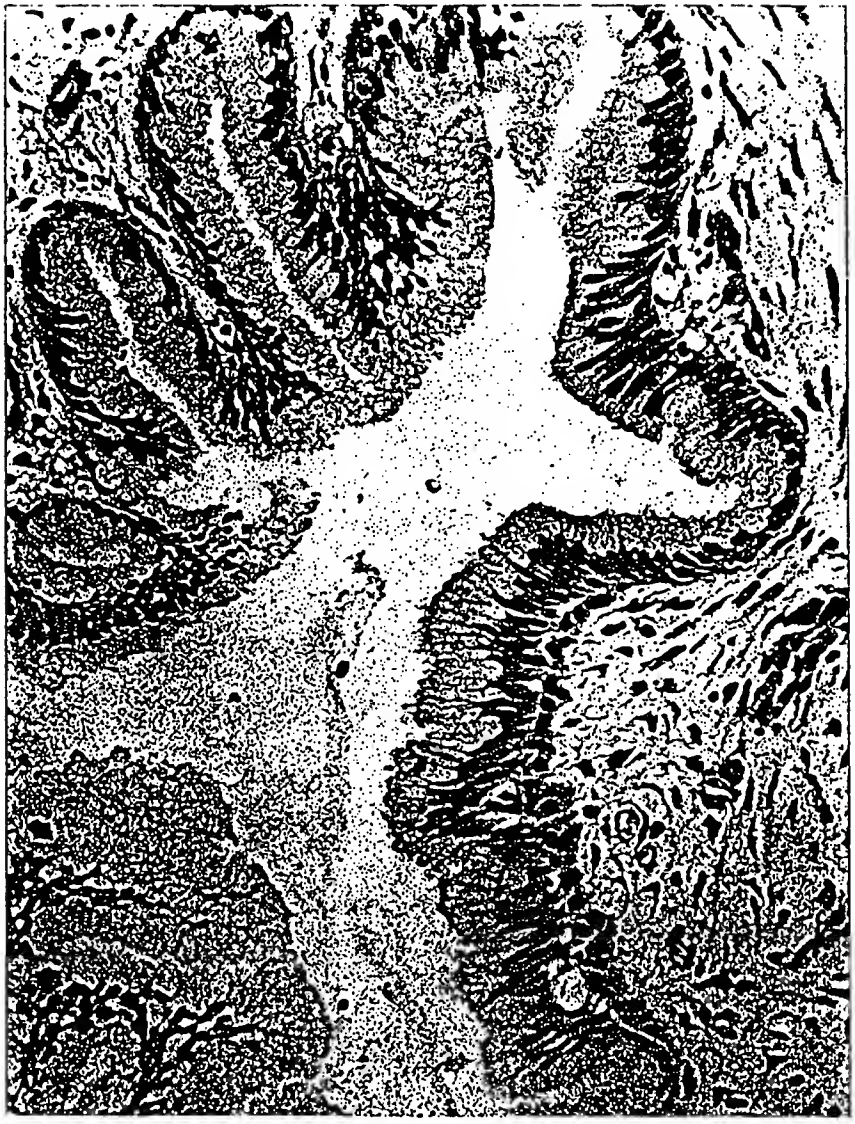

FIG. 17

```
        10         20         30         40         50         60         70         80         90
         *          *          *          *          *          *          *          *          *
GGAATTCCGC CCGCCCTGCG CCCCGCTCTG CTGTGGGCGC TGCTGGCGCT CTGGCTGTGC TGCGCGGCCC CCGCGCATGC ATTGCAGTGT
            P  A  L  R  P  A  L  L  W  A  L  L  A  L  W  L  C  C  A  A  P  A  H  A  L  Q  C>

       100        110        120        130        140        150        160        170        180
         *          *          *          *          *          *          *          *          *
CGAGATGGCT ATGAACCCTG TGTAAATGAA GGAATGTGTG TTACCTACCA CAATGGCACA GGATACTGCA AATGTCCAGA AGGCTTCTTG
 R  D  G  Y  E  P  C  V  N  E  G  M  C  V  T  Y  H  N  G  T  G  Y  C  K  C  P  E  G  F  L>

       190        200        210        220        230        240        250        260        270
         *          *          *          *          *          *          *          *          *
GGGGAATATT GTCAACATCG AGACCCCTGT GAGAAGAACC GCTGCCAGAA TGGTGGGACT TGTGTGGCCC AGGCCATGCT GGGGAAAGCC
 G  E  Y  C  Q  H  R  D  P  C  E  K  N  R  C  Q  N  G  G  T  C  V  A  Q  A  M  L  G  K  A>

       280        290        300        310        320        330        340        350        360
         *          *          *          *          *          *          *          *          *
ACGTGCCGAT GTGCCTCAGG GTTTACAGGA GAGGACTGCC AGTACTCAAC ATCTCATCCA TGCTTTGTGT CTCGACCCTG CCTGAATGGC
 T  C  R  C  A  S  G  F  T  G  E  D  C  Q  Y  S  T  S  H  P  C  F  V  S  R  P  C  L  N  G>

       370        380        390        400        410        420        430        440        450
         *          *          *          *          *          *          *          *          *
GGCACATGCC ATATGCTCAG CCGGGATACC TATGAGTGCA CCTGTCAAGT CGGGTTTACA GGTAAGGAGT GCCAATGGAC GGATGCCTGC
 G  T  C  H  M  L  S  R  D  T  Y  E  C  T  C  Q  V  G  F  T  G  K  E  C  Q  W  T  D  A  C>

       460        470        480        490        500        510        520        530        540
         *          *          *          *          *          *          *          *          *
CTGTCTCATC CCTGTGCAAA TGGAAGTACC TGTACCACTG TGGCCAACCA GTTCTCCTGC AAATGCCTCA CAGGCTTCAC AGGGCAGAAA
 L  S  H  P  C  A  N  G  S  T  C  T  T  V  A  N  Q  F  S  C  K  C  L  T  G  F  T  G  Q  K>

       550        560        570        580        590        600        610        620        630
         *          *          *          *          *          *          *          *          *
TGTGAGACTG ATGTCAATGA GTGTGACATT CCAGGACACT GCCAGCATGG TGGCACCTGC CTCAACCTGC CTGGTTCCTA CCAGTGCCAG
 C  E  T  D  V  N  E  C  D  I  P  G  H  C  Q  H  G  G  T  C  L  N  L  P  G  S  Y  Q  C  Q>

       640        650        660        670        680        690        700        710        720
         *          *          *          *          *          *          *          *          *
TGCCCTCAGG GCTTCACAGG CCAGTACTGT GACAGCCTGT ATGTGCCCTG TGCACCCTCA CCTTGTGTCA ATGGAGGCAC CTGTCGGCAG
 C  P  Q  G  F  T  G  Q  Y  C  D  S  L  Y  V  P  C  A  P  S  P  C  V  N  G  G  T  C  R  Q>

       730        740        750        760        770        780        790        800        810
         *          *          *          *          *          *          *          *          *
ACTGGTGACT TCACTTTTGA GTGCAACTGC CTTCCAGGTT TTGAAGGGAG CACCTGTGAG AGGAATATTG ATGACTGCCC TAACCACAGG
 T  G  D  F  T  F  E  C  N  C  L  P  G  F  E  G  S  T  C  E  R  N  I  D  D  C  P  N  H  R>
```

FIG. 17 CONT'D

```
      820       830       840       850       860       870       880       890       900
       *         *         *         *         *         *         *         *         *
TGTCAGAATG GAGGGGTTTG TGTGGATGGG GTCAACACTT ACAACTGCCG CTGTCCCCCA CAATGACAG GACAGTTCTG CACAGAGGAT
 C Q N  G G V C  V D G  V N T  Y N C R  C P P  Q W T  G Q F C  T E D>

       910       920       930       940       950       960       970       980       990
       *         *         *         *         *         *         *         *         *
GTGGATGAAT GCCTGCTGCA GCCCAATGCC TGTCAAAATG GGGCACCTG TGCCAACCGC AATGGAGGCT ATGGCTGTGT ATGTGTCAAC
 V D E  C L L Q  P N A  C Q N  G G T C  A N R  N G G  Y G C V  C V N>

      1000      1010      1020      1030      1040      1050      1060      1070      1080
       *         *         *         *         *         *         *         *         *
GGCTGGAGTG GAGATGACTG CAGTGAGAAC ATTGATGATT GTGCCTTCGC CTCCTGTACT CCAGGCTCCA CCTGCATCGA CCGTGTGCCC
 G W S  G D D C  S E N  I D D  C A F A  S C T  P G S  T C I D  R V A>

      1090      1100      1110      1120      1130      1140      1150      1160      1170
       *         *         *         *         *         *         *         *         *
TCCTTCTCTT GCATGTGCCC AGAGGGGAAG GCAGGTCTCC TGTGTCATCT GGATGATGCA TGCATCAGCA ATCCTTGCCA CAAGGGGCCA
 S F S  C M C P  E G K  A G L  L C H L  D D A  C I S  N P C B  K G A>

      1180      1190      1200      1210      1220      1230      1240      1250      1260
       *         *         *         *         *         *         *         *         *
CTGTGTGACA CCAACCCCCT AAATGGGCAA TATATTTGCA CCTGCCCACA AGGCTACAAA GGGGCTGACT GCACAGAAGA TGTGGATGAA
 L C D  T N P L  N G Q  Y I C  T C P Q  G Y K  G A D  C T E D  V D E>

      1270      1280      1290      1300      1310      1320      1330      1340      1350
       *         *         *         *         *         *         *         *         *
TGTGCCATGG CCAATAGCAA TCCTTGTGAG CATGCAGGAA AATGTGTGAA CACGGATGGC GCCTTCCACT GTGAGTGTCT GAAGGGTTAT
 C A M  A N S N  P C E  H A G  K C V N  T D G  A F H  C E C L  K G Y>

      1360      1370      1380      1390      1400      1410      1420      1430      1440
       *         *         *         *         *         *         *         *         *
GCAGGACCTC GTTGTGAGAT GGACATCAAT GAGTGCCATT CAGACCCCTG CCAGAATGAT GCTACCTGTC TGGATAAGAT TGGAGGCTTC
 A G P  R C E M  D I N  E C H  S D P C  Q N D  A T C  L D K I  G G F>

      1450      1460      1470      1480      1490      1500      1510      1520      1530
       *         *         *         *         *         *         *         *         *
ACATGTCTGT GCATGCCAGG TTTCAAAGGT GTGCATTGTG AATTAGAAAT AAATGAATGT CAGAGCAACC CTTGTGTGAA CAATGGGCAG
 T C L  C M P G  F K G  V H C  E L E I  N E C  Q S N  P C V N  N G Q>

      1540      1550      1560      1570      1580      1590      1600      1610      1620
       *         *         *         *         *         *         *         *         *
TGTGTGGATA AAGTCAATCG TTTCCAGTGC CTGTGTCCTC CTGGTTTCAC TGGGCCAGTT TGCCAGATTG ATATTGATGA CTGTTCCAGT
 C V D  K V N R  F Q C  L C P  P G F T  G P V  C Q I  D I D D  C S S>
```

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FIG. 17 CONT'D

```
      1630       1640       1650       1660       1670       1680       1690       1700       1710
         *          *          *          *          *          *          *          *          *
ACTCCGTGTC TGAATGGGGC AAAGTGTATC GATCACCCGA ATGGCTATGA ATGCCAGTGT GCCACAGGTT TCACTGGTGT GTTGTGTGAG
 T  P  C   L  N  G  A   K  C  I   D  H  P   N  G  Y  E   C  Q  C   A  T  G   F  T  G  V   L  C  E>

      1720       1730       1740       1750       1760       1770       1780       1790       1800
         *          *          *          *          *          *          *          *          *
GAGAACATTG ACAACTGTGA CCCCGATCCT TGCCACCATG GTCAGTGTCA GGATGGTATT GATTCCTACA CCTGCATCTG CAATCCCGGG
 E  N  I   D  N  C  D   P  D  P   C  H  H   G  Q  C  Q   D  G  I   D  S  Y   T  C  I  C   N  P  G>

      1810       1820       1830       1840       1850       1860       1870       1880       1890
         *          *          *          *          *          *          *          *          *
TACATGGGCG CCATCTGCAG TGACCAGATT GATGAATGTT ACAGCAGCCC TTGCCTGAAC GATGGTCGCT GCATTGACCT GGTCAATGGC
 Y  M  G   A  I  C  S   D  Q  I   D  E  C   Y  S  S  P   C  L  N   D  G  R   C  I  D  L   V  N  G>

      1900       1910       1920       1930       1940       1950       1960       1970       1980
         *          *          *          *          *          *          *          *          *
TACCAGTGCA ACTGCCAGCC AGGCACGTCA GGGGTTAATT GTGAAATTAA TTTTGATGAC TGTGCAAGTA ACCCTTGTAT CCATGGAATC
 Y  Q  C   N  C  Q  P   G  T  S   G  V  N   C  E  I  N   F  D  D   C  A  S   N  P  C  I   H  G  I>

      1990       2000       2010       2020       2030       2040       2050       2060       2070
         *          *          *          *          *          *          *          *          *
TGTATGGATG GCATTAATCG CTACAGTTGT GTCTGCTCAC CAGGATTCAC AGGGCAGAGA TGTAACATTG ACATTGATGA GTGTGCCTCC
 C  M  D   G  I  N  R   Y  S  C   V  C  S   P  G  F  T   G  Q  R   C  N  I   D  I  D  E   C  A  S>

      2080       2090       2100       2110       2120       2130       2140       2150       2160
         *          *          *          *          *          *          *          *          *
AATCCCTGTC GCAAGGGTGC AACATGTATC AACGGTGTGA ATGGTTTCCG CTGTATATGC CCCGAGGGAC CCCATCACCC CAGCTGCTAC
 N  P  C   R  K  G  A   T  C  I   N  G  V   N  G  F  R   C  I  C   P  E  G   P  H  H  P   S  C  Y>

      2170       2180       2190       2200       2210       2220       2230       2240       2250
         *          *          *          *          *          *          *          *          *
TCACAGGTGA ACGAATGCCT GAGCAATCCC TGCATCCATG GAAACTGTAC TGGAGGTCTC AGTGGATATA AGTGTCTCTG TGATGCAGGC
 S  Q  V   N  E  C  L   S  N  P   C  I  H   G  N  C  T   G  G  L   S  G  Y   K  C  L  C   D  A  G>

      2260       2270       2280       2290       2300       2310       2320       2330       2340
         *          *          *          *          *          *          *          *          *
TGGGTTGGCA TCAACTGTGA AGTGGACAAA AATGAATGCC TTTCGAATCC ATGCCAGAAT GGAGGAACTT GTGACAATCT GGTGAATGGA
 W  V  G   I  N  C  E   V  D  K   N  E  C   L  S  N  P   C  Q  N   G  G  T   C  D  N  L   V  N  G>

      2350       2360       2370       2380       2390       2400       2410       2420       2430
         *          *          *          *          *          *          *          *          *
TACAGGTGTA CTTGCAAGAA GGGCTTTAAA GGCTATAACT GCCAGGTGAA TATTGATGAA TGTGCCTCAA ATCCATGCCT GAACCAAGGA
 Y  R  C   T  C  K  F   G  F  K   G  Y  N   C  Q  V  N   I  D  E   C  A  S   N  P  C  L   N  Q  G>

      2440       2450       2460       2470       2480       2490       2500       2510       2520
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FIG. 17 CONT'D

```
         *         *         *         *         *         *         *         *         *
ACCTGCTTTG ATGACATAAG TGGCTACACT TGCCACTGTG TGCTGCCATA CACAGGCAAG AATTGTCAGA CAGTATTGGC TCCCTGTTCC
 T  C  F   D  D  I  S   G  Y  T   C  H  C   V  L  P  Y   T  G  K   N  C  Q   T  V  L  A   P  C  S>
      2530      2540      2550      2560      2570      2580      2590      2600      2610
         *         *         *         *         *         *         *         *         *
CCAAACCCTT GTGAGAATGC TGCTGTTTGC AAAGAGTCAC CAAATTTTGA GAGTTATACT TGCTTGTGTG CTCCTGGCTG GCAAGGTCAG
 P  N  P   C  E  N  A   A  V  C   K  E  S   P  N  F  E   S  Y  T   C  L  C   A  P  G  W   Q  G  Q>
      2620      2630      2640      2650      2660      2670      2680      2690      2700
         *         *         *         *         *         *         *         *         *
CGGTGTACCA TTGACATTGA CGAGTGTATC TCCAAGCCCT GCATGAACCA TGGTCTCTGC CATAACACCC AGGGCAGCTA CATGTGTGAA
 R  C  T   I  D  I  D   E  C  I   S  K  P   C  M  N  H   G  L  C   H  N  T   Q  G  S  Y   M  C  E>
      2710      2720      2730      2740      2750      2760      2770      2780      2790
         *         *         *         *         *         *         *         *         *
TGTCCACCAG GCTTCAGTGG TATGGACTGT GAGGAGGACA TTGATGACTG CCTTGCCAAT CCTTGCCAGA ATGGAGGTTC CTGTATGGAT
 C  P  P   G  F  S  G   M  D  C   E  E  D   I  D  D  C   L  A  N   P  C  Q   N  G  G  S   C  M  D>
      2800      2810      2820      2830      2840      2850      2860      2870      2880
         *         *         *         *         *         *         *         *         *
GGAGTGAATA CTTTCTCCTG CCTCTGCCTT CCGGGTTTCA CTGGGGATAA GTGCCAGACA GACATGAATG AGTGTCTGAG TGAACCCTGT
 G  V  N   T  F  S  C   L  C  L   P  G  F   T  G  D  K   C  Q  T   D  M  N   E  C  L  S   E  P  C>
      2890      2900      2910      2920      2930      2940      2950      2960      2970
         *         *         *         *         *         *         *         *         *
AAGAATGGAG GGACCTGCTC TGACTACGTC AACAGTTACA CTTGCAAGTG CCAGGCAGGA TTTGATGGAG TCCATTGTGA GAACAACATC
 K  N  G   G  T  C  S   D  Y  V   N  S  Y   T  C  K  C   Q  A  G   F  D  G   V  H  C  E   N  N  I>
      2980      2990      3000      3010      3020      3030      3040      3050      3060
         *         *         *         *         *         *         *         *         *
AATGAGTGCA CTGAGAGCTC CTGTTTCAAT GGTGGCACAT GTGTTGATGG GATTAACTCC TTCTCTTGCT TGTGCCCTGT GGGTTTCACT
 N  E  C   T  E  S  S   C  F  N   G  G  T   C  V  D  G   I  N  S   F  S  C   L  C  P  V   G  F  T>
      3070      3080      3090      3100      3110      3120      3130      3140      3150
         *         *         *         *         *         *         *         *         *
GGATCCTTCT GCCTCCATGA GATCAATGAA TGCAGCTCTC ATCCATGCCT GAATGAGGGA ACGTGTGTTG ATGGCCTGGG TACCTACCGC
 G  S  F   C  L  H  E   I  N  E   C  S  S   H  P  C  L   N  E  G   T  C  V   D  G  L  G   T  Y  R>
      3160      3170      3180      3190      3200      3210      3220      3230      3240
         *         *         *         *         *         *         *         *         *
TGCAGCTGCC CCCTGGGCTA CACTGGGAAA AACTGTCAGA CCCTGGTGAA TCTCTGCAGT CGGTCTCCAT GTAAAAACAA AGGTACTTGT
 C  S  C   P  L  G  Y   T  G  K   N  C  Q   T  L  V  N   L  C  S   R  S  P   C  K  N  K   G  T  C>
      3250      3260      3270      3280      3290      3300      3310      3320      3330
         *         *         *         *         *         *         *         *         *
```

FIG. 17 CONT'D

```
GTTCAGAAAA AAGCAGAGTC CCAGTGCCTA TGTCCATCTG GATGGGCTGG TGCCTATTGT GACGTGCCCA ATGTCTCTTG TGACATAGCA
V Q K K A E S Q C L C P S G W A G A Y C D V P N V S C D I A>
      3340       3350       3360       3370       3380       3390       3400       3410       3420
       *          *          *          *          *          *          *          *          *
GCCTCCAGGA GAGGTGTGCT TGTTGAACAC TTGTGCCAGC ACTCAGGTGT CTGCATCAAT GCTGGCAACA CGCATTACTG TCAGTGCCCC
A S R R G V L V E H L C Q H S G V C I N A G N T H Y C Q C P>
      3430       3440       3450       3460       3470       3480       3490       3500       3510
       *          *          *          *          *          *          *          *          *
CTGGGCTATA CTGGGAGCTA CTGTGAGGAG CAACTCGATG AGTGTGCGTC CAACCCCTGC CAGCACGGGG CAACATGCAG TGACTTCATT
L G Y T G S Y C E E Q L D E C A S N P C Q H G A T C S D F I>
      3520       3530       3540       3550       3560       3570       3580       3590       3600
       *          *          *          *          *          *          *          *          *
GGTGGATACA GATGCGAGTG TGTCCCAGGC TATCAGGGTG TCAACTGTGA GTATGAAGTG GATGAGTGCC AGAATCAGCC CTGCCAGAAT
G G Y R C E C V P G Y Q G V N C E Y E V D E C Q N Q P C Q N>
      3610       3620       3630       3640       3650       3660       3670       3680       3690
       *          *          *          *          *          *          *          *          *
GGAGGCACCT GTATTGACCT TGTGAACCAT TTCAAGTGCT CTTGCCCACC AGGCACTCGG GGCCTACTCT GTGAAGAGAA CATTGATGAC
G G T C I D L V N H F K C S C P P G T R G L L C E E N I D D>
      3700       3710       3720       3730       3740       3750       3760       3770       3780
       *          *          *          *          *          *          *          *          *
TGTGCCCGGG GTCCCCATTG CCTTAATGGT GGTCAGTGCA TGGATAGGAT TGGAGGCTAC AGTTGTGCCT GCTTGCCTGG CTTTGCTGGG
C A R G G P H C L N G G Q C M D R I G G G Y S C R C L P G F A G>
      3790       3800       3810       3820       3830       3840       3850       3860       3870
       *          *          *          *          *          *          *          *          *
GAGCGTTGTG AGGGAGACAT CAACGAGTGC CTCTCCAACC CCTGCAGCTC TGAGGGCAGC CTGGACTGTA TACAGCTCAC CAATGACTAC
E R C E G D I N E C L S N P C S S E G S L D C I Q L T N D Y>
      3880       3890       3900       3910       3920       3930       3940       3950       3960
       *          *          *          *          *          *          *          *          *
CTGTGTGTTT GCCGTAGTGC CTTTACTGGC CGGCACTGTG AAACCTCGT CGATGTGTGT CCCCAGATGC CCTGCCTGAA TGGAGGGACT
L C V C R S A F T G R H C E T F V D V C P Q M P C L N G G T>
      3970       3980       3990       4000       4010       4020       4030       4040       4050
       *          *          *          *          *          *          *          *          *
TGTGCTGTGG CCAGTAACAT GCCTGATGGT TTCATTTGCC GTTGTCCCCC GGGATTTTCC GGGGCAAGGT GCCAGAGCAG CTGTGGACAA
C A V A S N M P D G F I C R C P P G F S G A R C Q S S C G Q>
      4060       4070       4080       4090       4100       4110       4120       4130       4140
       *          *          *          *          *          *          *          *          *
GTGAAATGTA GGAAGGGGGA GCAGTGTGTG CACACCGCCT CTGGACCCCG CTGCTTCTGC CCCAGTCCCC GGGACTGCGA GTCAGGCTGT
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FIG. 17 CONT'D

```
V K C R K G E Q C V H T A S G P R C F C P S P R D C E S G C>
                4150       4160       4170       4180       4190       4200       4210       4220       4230
                 *          *          *          *          *          *          *          *          *
GCCAGTAGCC CCTGCCAGCA CGGGGGCAGC TGCCACCCTC AGCGCCAGCC TCCTTATTAC TCCTGCCAGT GTGCCCCACC ATTCTCGGGT
A S S P C Q H G G S C B P Q R Q P P Y Y S C Q C A P P F S G>
                4240       4250       4260       4270       4280       4290       4300       4310       4320
                 *          *          *          *          *          *          *          *          *
AGCCGCTGTG AACTCTACAC GGCACCCCCC AGCACCCCTC CTGCCACCTG TCTGAGCCAG TATTGTGCCG ACAAAGCTCG GGATGCGGTC
S R C E L Y Y T A P P S T P P A T C L S Q Y C A D R A R D G V>
                4330       4340       4350       4360       4370       4380       4390       4400       4410
                 *          *          *          *          *          *          *          *          *
TGTGATGAGG CCTGCAACAG CCATGCCCTGC CAGTGGGATG GGGGTGACTG TTCTCTCACC ATGGAGAACC CCTGGGCCAA CTGCTCCTCC
C D E A C N S H A C Q W D G G D C S L T M E N P W A N C S S>
                4420       4430       4440       4450       4460       4470       4480       4490       4500
                 *          *          *          *          *          *          *          *          *
CCACTTCCCT GCTGGGATTA TATCAACAAC CAGTGTGATG AGCTGTGCAA CACGGTCGAG TGCCTGTTTG ACAACTTTGA ATGCCAGGGG
P L P C W D Y I N N Q C D E L C N T V E C L F D N F E C Q G>
                4510       4520       4530       4540       4550       4560       4570       4580       4590
                 *          *          *          *          *          *          *          *          *
AACAGCAAGA CATGCAAGTA TGACAAATAC TGTGCAGACC ACTTCAAAGA CAACCACTGT AACCAGGGGT GCAACAGTGA GGAGTGTGGT
N S K T C K Y D K Y C A D H F K D N H C N Q G C N S E E C G>
                4600       4610       4620       4630       4640       4650       4660       4670       4680
                 *          *          *          *          *          *          *          *          *
TGGGATGGGC TGGACTGTGC TGCTGACCAA CCTGAGAACC TGGCAGAAGG TACCCTGGTT ATTGTGGTAT TGATGCCACC TGAACAACTG
W D G L D C A A D Q P E N L A E G T L V I V V L M P P E Q L>
                4690       4700       4710       4720       4730       4740       4750       4760       4770
                 *          *          *          *          *          *          *          *          *
CTCCAGGATG CTCGCAGCTT CTTGCGGGCA CTGGGTACCC TGCTCCACAC CAACCTGCGC ATTAAGCGGG ACTCCCAGGG GGAACTCATG
L Q D A R S F L R A L G T L L H T N L R I K R D S Q G E L M>
                4780       4790       4800       4810       4820       4830       4840       4850       4860
                 *          *          *          *          *          *          *          *          *
GTGTACCCCT ATTATGGTGA GAAGTCAGCT GCTATGAAGA AACAGAGGAT GACACGCAGA TCCCTTCCTG GTGAACAGA ACAGGAGGTG
V Y P Y Y G E K S A A M K K Q R M T R R S L P G E Q E Q E V>
                4870       4880       4890       4900       4910       4920       4930       4940       4950
                 *          *          *          *          *          *          *          *          *
C[illegible]
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FIG. 17 CONT'D

```
      4960       4970       4980       4990       5000       5010       5020       5030       5040
         *          *          *          *          *          *          *          *          *
CTCCTGGCCT CTCACGCCAT ACAGGGGACC CTGTCATACC CTCTTGTGTC TGTCGTCAGT GAATCCCTGA CTCCAGAACG CACTCAGCTC
L  L  A   S  H  A  I   Q  G  T   L  S  Y   P  L  V  S   V  V  S   E  S  L   T  P  E  R   T  Q  L>

      5050       5060       5070       5080       5090       5100       5110       5120       5130
         *          *          *          *          *          *          *          *          *
CTCTATCTCC TTGCTGTTGC TGTTGTCATC ATTCTGTTTA TTATTCTGCT GGGGGTAATC ATGGCAAAAC GAAAGCGTAA GCATGGCTCT
L  Y  L   L  A  V  A   V  V  I   I  L  F   I  I  L  L   G  V  I   M  A  K   R  K  R  K   H  G  S>

      5140       5150       5160       5170       5180       5190       5200       5210       5220
         *          *          *          *          *          *          *          *          *
CTCTGGCTGC CTGAAGGTTT CACTCTTCGC CGAGATGCAA GCAATCACAA GCGTCGTGAG CCAGTGGGAC AGGATGCTGT GGGGCTGAAA
L  W  L   P  E  G  F   T  L  R   R  D  A   S  N  H  K   R  R  E   P  V  G   Q  D  A  V   G  L  K>

      5230       5240       5250       5260       5270       5280       5290       5300       5310
         *          *          *          *          *          *          *          *          *
AATCTCTCAG TGCAAGTCTC AGAAGCTAAC CTAATTGGTA CTGGAACAAG TGAACACTGG GTCGATGATG AAGGGCCCCA GCCAAAGAAA
N  L  S   V  Q  V  S   E  A  N   L  I  G   T  G  T  S   E  H  W   V  D  D   E  G  P  Q   P  K  K>

      5320       5330       5340       5350       5360       5370       5380       5390       5400
         *          *          *          *          *          *          *          *          *
GTAAAGGCTG AAGATGAGGC CTTACTCTCA GAAGAAGATG ACCCCATTGA TCGACGGCCA TGGACACAGC AGCACCTTGA AGCTGCAGAC
V  K  A   E  D  E  A   L  L  S   E  E  D   D  P  I  D   R  R  P   W  T  Q   Q  H  L  E   A  A  D>

      5410       5420       5430       5440       5450       5460       5470       5480       5490
         *          *          *          *          *          *          *          *          *
ATCCGTAGGA CACCATCGCT GGCTCTCACC CCTCCTCAGG CAGAGCAGGA GGTGGATGTG TTAGATGTGA ATGTCCGTGG CCCAGATGGC
I  R  R   T  P  S  L   A  L  T   P  P  Q   A  E  Q  E   V  D  V   L  D  V   N  V  R  G   P  D  G>

      5500       5510       5520       5530       5540       5550       5560       5570       5580
         *          *          *          *          *          *          *          *          *
TGCACCCCAT TGATGTTGGC TTCTCTCCGA GGAGGCAGCT CAGATTTGAG TGATGAAGAT GAAGATGCAG AGGACTCTTC TGCTAACATC
C  T  P   L  M  L  A   S  L  R   G  G  S   S  D  L  S   D  E  D   E  D  A   E  D  S  S   A  N  I>

      5590       5600       5610       5620       5630       5640       5650       5660       5670
         *          *          *          *          *          *          *          *          *
ATCACAGACT TGGTCTACCA GGGTGCCAGC CTCCAGGCCC AGACAGACCG GACTGGTGAG ATGGCCCTGC ACCTTGCAGC CCGCTACTCA
I  T  D   L  V  Y  Q   G  A  S   L  Q  A   Q  T  D  R   T  G  E   M  A  L   H  L  A  A   R  Y  S>

      5680       5690       5700       5710       5720       5730       5740       5750       5760
         *          *          *          *          *          *          *          *          *
CGGGCTGATG CTGCCAAGCG TCTCCTGGAT GCAGGTGCAG ATGCCAATGC CCAGGACAAC ATGGGCCGCT GTCCACTCCA TGCTGCAGTG
R  A  D   A  A  K  R   L  L  D   A  G  A   D  A  N  A   Q  D  N   M  G  R   C  P  L  H   A  A  V>
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FIG. 17 CONT'D

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      5770       5780       5790       5800       5810       5820       5830       5840       5850
         *          *          *          *          *          *          *          *          *
GCAGCTGATG CCCAAGGTGT CTTCCAGATT CTGATTCGCA ACCGAGTAAC TGATCTAGAT GCCAGGATGA ATGATGGTAC TACACCCCTG
A  A  D   A  Q  G  V   F  Q  I   L  I  R   N  R  V  T   D  L  D   A  R  M   N  D  G  T   T  P  L>

      5860       5870       5880       5890       5900       5910       5920       5930       5940
         *          *          *          *          *          *          *          *          *
ATCCTGGCTG CCCGCCTGGC TGTGGAGGGA ATGGTGGCAG AACTGATCAA CTGCCAAGCG GATGTGAATG CAGTGGATGA CCATGGAAAA
I  L  A   A  R  L  A   V  E  G   M  V  A   E  L  I  N   C  Q  A   D  V  N   A  V  D  D   H  G  K>

      5950       5960       5970       5980       5990       6000       6010       6020       6030
         *          *          *          *          *          *          *          *          *
TCTGCTCTTC ACTGGGCAGC TGCTGTCAAT AATGTGGAGG CAACTCTTTT GTTGTTGAAA AATGGGGCCA ACCGAGACAT GCAGGACAAC
S  A  L   H  W  A  A   A  V  N   N  V  E   A  T  L  L   L  L  K   N  G  A   N  R  D  M   Q  D  N>

      6040       6050       6060       6070       6080       6090       6100       6110       6120
         *          *          *          *          *          *          *          *          *
AAGGAAGAGA CACCTCTGTT TCTTGCTGCC CGGGAGGGGA GCTATGAAGC AGCCAAGATC CTGTTAGACC ATTTTGCCAA TCGAGACATC
K  E  E   T  P  L  F   L  A  A   R  E  G   S  Y  E  A   A  K  I   L  L  D   H  F  A  N   R  D  I>

      6130       6140       6150       6160       6170       6180       6190       6200       6210
         *          *          *          *          *          *          *          *          *
ACAGACCATA TGGATCGTCT TCCCCGGGAT GTGGCTCGGG ATCGCATGCA CCATGACATT GTGCGCCTTC TGGATGAATA CAATGTGACC
T  D  H   M  D  R  L   P  R  D   V  A  R   D  R  M  H   H  D  I   V  R  L   L  D  E  Y   N  V  T>

      6220       6230       6240       6250       6260       6270       6280       6290       6300
         *          *          *          *          *          *          *          *          *
CCAAGCCCTC CAGGCACCGT GTTGACTTCT GCTCTCTCAC CTGTCATCTG TGGGCCCAAC AGATCTTTCC TCAGCCTGAA GCACACCCCA
P  S  P   P  G  T  V   L  T  S   A  L  S   P  V  I  C   G  P  N   R  S  F   L  S  L  K   H  T  P>

      6310       6320       6330       6340       6350       6360       6370       6380       6390
         *          *          *          *          *          *          *          *          *
ATGGGCAAGA AGTCTAGACG GCGCAGTGCC AAGAGTACCA TGCCTACTAG CCTCCCTAAC CTTGCCAAGG AGGCAAAGGA TGCCAAGGGT
M  G  K   K  S  R  R   P  S  A   K  S  T   M  P  T  S   L  P  N   L  A  K   E  A  K  D   A  K  G>

      6400       6410       6420       6430       6440       6450       6460       6470       6480
         *          *          *          *          *          *          *          *          *
AGTAGGAGGA AGAAGTCTCT GAGTGAGAAG GTCCAACTGT CTGAGAGTTC AGTAACTTTA TCCCCTGTTG ATTCCCTAGA ATCTCCTCAC
S  R  R   K  K  S  L   S  E  K   V  Q  L   S  E  S  S   V  T  L   S  P  V   D  S  L  E   S  P  H>

      6490       6500       6510       6520       6530       6540       6550       6560       6570
         *          *          *          *          *          *          *          *          *
ACGTATGTTT CCGACACCAC ATCCTCTCCA ATGATTACAT CCCCTGGGAT CTTACAGGCC TCACCCAACC CTATGTTGGC CACTGCCGCC
T  Y  V   S  D  T  T   S  S  P   M  I  T   S  P  G  I   L  Q  A   S  P  N   P  M  L  A   T  A  A>

      6580       6590       6600       6610       6620       6630       6640       6650       6660
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FIG. 17 CONT'D

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           *          *          *          *          *          *          *          *          *
CCTCCTGCCC CAGTCCATGC CCAGCATGCA CTATCTTTTT CTAACCTTCA TGAAATGCAG CCTTTGGCAC ATGGGGCCAG CACTGTGCTT
P  P  A    P  V  H  A   Q  H  A   L  S  F   S  N  L  H   E  M  Q   P  L  A   H  G  A  S   T  V  L>
      6670       6680       6690       6700       6710       6720       6730       6740       6750
           *          *          *          *          *          *          *          *          *
CCCTCAGTGA GCCAGTTGCT ATCCCACCAC CACATTGTGT CTCCAGGCAG TGGCAGTGCT GGAAGCTTGA GTAGGCTCCA TCCAGTCCCA
P  S  V    S  Q  L  L   S  H  H   H  I  V   S  P  G  S   G  S  A   G  S  L   S  R  L  H   P  V  P>
      6760       6770       6780       6790       6800       6810       6820       6830       6840
           *          *          *          *          *          *          *          *          *
GTCCCAGCAG ATTGGATGAA CCGCATGGAG GTGAATGAGA CCCAGTACAA TGAGATGTTT GGTATGGTCC TGGCTCCAGC TGAGGGCACC
V  P  A    D  W  M  N   R  M  E   V  N  E   T  Q  Y  N   E  M  F   G  M  V   L  A  P  A   E  G  T>
      6850       6860       6870       6880       6890       6900       6910       6920       6930
           *          *          *          *          *          *          *          *          *
CATCCTGGCA TAGCTCCCCA GAGCAGGCCA CCTGAAGGGA AGCACATAAC CACCCCTCGG GAGCCCTTGC CCCCCATTGT GACTTTCCAG
H  P  G    I  A  P  Q   S  R  P   P  E  G   K  H  I  T   T  P  R   E  P  L   P  P  I  V   T  F  Q>
      6940       6950       6960       6970       6980       6990       7000       7010       7020
           *          *          *          *          *          *          *          *          *
CTCATCCCTA AAGGCAGTAT TGCCCAACCA GCGGGGGCTC CCCAGCCTCA GTCCACCTGC CCTCCAGCTG TTGCGGGCCC CCTGCCCACC
L  I  P    K  G  S  I   A  Q  P   A  G  A   P  Q  P  Q   S  T  C   P  P  A   V  A  G  P   L  P  T>
      7030       7040       7050       7060       7070       7080       7090       7100       7110
           *          *          *          *          *          *          *          *          *
ATGTACCAGA TTCCAGAAAT GGCCCGTTTG CCCAGTGTGG CTTTCCCCAC TGCCATGATG CCCCAGCAGG ACGGGCAGGT AGCTCAGACC
M  Y  Q    I  P  E  M   A  R  L   P  S  V   A  F  P  T   A  M  M   P  Q  Q   D  G  Q  V   A  Q  T>
      7120       7130       7140       7150       7160       7170       7180       7190       7200
           *          *          *          *          *          *          *          *          *
ATTCTCCCAG CCTATCATCC TTTCCCAGCC TCTGTGGGCA AGTACCCCAC ACCCCCTTCA CAGCACAGTT ATGCTTCCTC AAATGCTGCT
I  L  P    A  Y  H  P   F /P  A   S  V  G   K  Y  P  T   P  P  S   Q  H  S   Y  A  S  S   N  A  A>
      7210       7220       7230       7240       7250       7260       7270       7280       7290
           *          *          *          *          *          *          *          *          *
GAGCGAACAC CCAGTCACAG TGGTCACCTC CAGGGTGAGC ATCCCTACCT GACACCATCC CCAGAGTCTC CTGACCAGTG GTCAAGTTCA
E  R  T    P  S  H  S   G  H  L   Q  G  E   H  P  Y  L   T  P  S   P  E  S   P  D  Q  W   S  S  S>
      7300       7310       7320       7330       7340       7350       7360       7370       7380
           *          *          *          *          *          *          *          *          *
TCACCCCACT CTGCTTCTGA CTGGTCAGAT GTGACCACCA GCCCTACCCC TGGGGGTGCT GGAGGAGGTC AGCGGGGACC TGGGACACAC
S  P  H    S  A  S  D   W  S  D   V  T  T   S  P  T  P   G  G  A   G  G  G   Q  R  G  P   G  T  H>
      7390       7400       7410       7420       7430       7440       7450       7460       7470
           *          *          *          *          *          *          *          *          *
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FIG. 17 CONT'D

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ATGTCTGAGC CACCACACAA CAACATGCAG GTTTATGCGT GAGAGAGTCC ACCTCCAGTG TAGAGACATA ACTGACTTTT GTAAATGCTG
 M  S  E   P  P  H  N   N  M  Q   V  Y  A>

      7480       7490       7500       7510       7520       7530       7540       7550       7560
         *          *          *          *          *          *          *          *          *
CTGAGGAACA AATGAAGGTC ATCCGGGAGA GAAATGAAGA AATCTCTGGA GCCAGCTTCT AGAGGTAGGA AAGAGAAGAT GTTCTTATTC

      7570       7580       7590       7600       7610       7620       7630       7640       7650
         *          *          *          *          *          *          *          *          *
AGATAATGCA AGAGAAGCAA TTCGTCAGTT TCACTGGGTA TCTGCAAGGC TTATTGATTA TTCTAATCTA ATAAGACAAG TTTGTGGAAA

      7660       7670       7680       7690       7700       7710       7720       7730       7740
         *          *          *          *          *          *          *          *          *
TGCAAGATGA ATACAAGCCT TGGGTCCATG TTTACTCTCT TCTATTTGGA GAATAAGATG GATGCTTATT GAAGCCCAGA CATTCTTGCA

      7750       7760       7770       7780       7790       7800       7810       7820       7830
         *          *          *          *          *          *          *          *          *
GCTTGGACTG CATTTTAAGC CCTGCAGGCT TCTGCCATAT CCATGAGAAG ATTCTACACT AGCGTCCTGT TGGGAATTAT GCCCTGGAAT

      7840       7850       7860       7870       7880       7890       7900       7910       7920
         *          *          *          *          *          *          *          *          *
TCTGCCTGAA TTGACCTACG CATCTCCTCC TCCTTGGACA TTCTTTTGTC TTCATTTGGT GCTTTTGGTT TTGCACCTCT CCGTGATTGT

      7930       7940       7950       7960       7970       7980       7990       8000       8010
         *          *          *          *          *          *          *          *          *
AGCCCTACCA GCATGTTATA GGGCAAGACC TTTGTGCTTT TGATCATTCT GGCCCATGAA AGCAACTTTG GTCTCCTTTC CCCTCCTGTC

      8020       8030       8040       8050       8060       8070       8080       8090       8100
         *          *          *          *          *          *          *          *          *
TTCCCGGTAT CCCTTGGAGT CTCACAAGGT TTACTTTGGT ATGGTTCTCA GCACAAACCT TTCAAGTATG TTGTTTCTTT GGAAAATGGA

      8110       8120       8130       8140       8150       8160       8170       8180       8190
         *          *          *          *          *          *          *          *          *
CATACTGTAT TGTGTTCTCC TGCATATATC ATTCCTGGAG AGAGAAGGGG AGAAGAATAC TTTTCTTCAA CAAATTTTGG GGGCAGGAGA

      8200       8210       8220       8230       8240       8250       8260       8270       8280
         *          *          *          *          *          *          *          *          *
TCCCTTCAAG AGGCTGCACC TTAATTTTTC TTGTCTGTGT GCAGGTCTTC ATATAAACTT TACCAGGAAG AAGGGTGTGA GTTTGTTGTT

      8290       8300       8310       8320       8330       8340       8350       8360       8370
         *          *          *          *          *          *          *          *          *
TTTCTGTGTA TGGGCCTGGT CAGTGTAAAG TTTTATCCTT GATAGTCTAG TTACTATGAC CCTCCCCACT TTTTTAAAAC CAGAAAAAGG

      8380       8390       8400       8410       8420       8430       8440       8450       8460
         *          *          *          *          *          *          *          *          *
TTTGGAATGT TGGAATGACC AAGAGACAAG TTAACTCGTG CAAGAGCCAG TTACCCACCC ACAGGTCCCC CTACTTCCTG CCAAGCATTC
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FIG. 17 CONT'D

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      8470       8480       8490       8500       8510       8520       8530       8540       8550
         *          *          *          *          *          *          *          *          *
CATTGACTGC CTGTATGGAA CACATTTGTC CCAGATCTGA GCATTCTAGG CCTGTTTCAC TCACTCACCC AGCATATGAA ACTAGTCTTA

      8560       8570       8580       8590       8600       8610       8620       8630       8640
         *          *          *          *          *          *          *          *          *
ACTGTTGAGC CTTTCCTTTC ATATCCACAG AAGACACTGT CTCAAATGTT GTACCCTTGC CATTTAGGAC TGAACTTTCC TTAGCCCAAG

      8650       8660       8670       8680       8690       8700       8710       8720       8730
         *          *          *          *          *          *          *          *          *
GGACCCAGTG ACAGTTGTCT TCCGTTTGTC AGATGATCAG TCTCTACTGA TTATCTTGCT GCTTAAAGGC CTGCTCACCA ATCTTTCTTT

      8740       8750       8760       8770       8780       8790       8800       8810       8820
         *          *          *          *          *          *          *          *          *
CACACCGTGT GGTCCGTGTT ACTGGTATAC CCAGTATGTT CTCACTGAAG ACATGGACTT TATATGTTCA AGTGCAGGAA TTGGAAAGTT

      8830       8840       8850       8860       8870       8880       8890       8900       8910
         *          *          *          *          *          *          *          *          *
GGACTTGTTT TCTATGATCC AAAACAGCCC TATAAGAAGG TTGGAAAAGG AGGAACTATA TAGCAGCCTT TGCTATTTTC TGCTACCATT

      8920       8930       8940       8950       8960       8970       8980       8990       9000
         *          *          *          *          *          *          *          *          *
TCTTTTCCTC TGAAGCGGCC ATGACATTCC CTTTGGCAAC TAACGTAGAA ACTCAACAGA ACATTTTCCT TTCCTAGAGT CACCTTTTAG

      9010       9020       9030       9040       9050       9060       9070       9080       9090
         *          *          *          *          *          *          *          *          *
ATGATAATGG ACAACTATAG ACTTGCTCAT TGTTCAGACT GATTGCCCCT CACCTGAATC CACTCTCTGT ATTCATGCTC TTGGCAATTT

      9100       9110       9120       9130       9140       9150       9160       9170       9180
         *          *          *          *          *          *          *          *          *
CTTTGACTTT CTTTTAAGGG CAGAAGCATT TTAGTTAATT GTAGATAAAG AATAGTTTTC TTCCTCTTCT CCTTGGGCCA GTTAATAATT

      9190       9200       9210       9220       9230       9240       9250       9260       9270
         *          *          *          *          *          *          *          *          *
GGTCCATGGC TACACTGCAA CTTCCGTCCA GTGCTGTGAT GCCCATGACA CCTGCAAAAT AAGTTCTGCC TGGGCATTTT GTAGATATTA

      9280       9290       9300       9310       9320       9330       9340       9350       9360
         *          *          *          *          *          *          *          *          *
ACAGGTGAAT TCCCGACTCT TTTGGTTTGA ATGACAGTTC TCATTCCTTC TATGGCTGCA AGTATGCATC AGTGCTTCCC ACTTACCTGA

      9370       9380       9390       9400       9410       9420       9430       9440       9450
         *          *          *          *          *          *          *          *          *
TTTGTCTGTC GGTGGCCCCA TATGGAAACC CTGCGTGTCT GTTGGCATAA TAGTTTACAA ATGGTTTTTT CAGTCCTATC CAAATTTATT

      9460       9470       9480       9490       9500       9510       9520       9530       9540
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FIG. 17 CONT'D

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         *          *          *          *          *          *          *          *          *
GAACCAACAA AAATAATTAC TTCTGCCCTG AGATAAGCAG ATTAAGTTTG TTCATTCTCT GCTTTATTCT CTCCATGTGG CAACATTCTG

      9550       9560       9570       9580       9590       9600       9610       9620       9630
         *          *          *          *          *          *          *          *          *
TCAGCCTCTT TCATAGTGTG CAAACATTTT ATCATTCTAA ATGGTGACTC TCTGCCCTTG GACCCATTTA TTATTCACAG ATGGGGAGAA

      9640       9650       9660       9670       9680       9690       9700       9710       9720
         *          *          *          *          *          *          *          *          *
CCTATCTGCA TGGACCCTCA CCATCCTCTG TGCAGCACAC ACAGTGCAGG GAGCCAGTGG CGATGGCGAT GACTTTCTTC CCCTGGGAAT

TCC
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